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(71) Applicant: ZYMOGENETICS, INC. [US/US]; 1201 Eastlake Avenue East, Seattle, WA 98102 (US).

(72) Inventors: DEISHER, Theresa, A.; 4006 Greenwood Avenue North, Seattle, WA 98103 (US). CONKLIN, Darrell, C.; Apartment 2, 2332 Minor Avenue East, Seattle, WA 98102 (US). RAYMOND, Fenella, C.; 3103 N.E. 85th Street, Seattle, WA 98115 (US). BUKOWSKI, Thomas, R.; 6259 Palatine Avenue North, Seattle, WA 98103 (US). HOLDERMAN, Susan, D.; 3712 101st Way N.E., Kirkland, WA 98033 (US). HANSEN, Brigit; Lake Union Terrace, 210 East Blaine Street #304, Seattle, WA 98102 (US). SHEPPARD, Paul, O.; 20717 N.E. 2nd Street, Redmond, WA 98053 (US).

(74) Agent: SAWISLAK, Deborah, A.; ZymoGenetics, Inc., 1201 Eastlake Avenue East, Seattle, WA 98102 (US).

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(57) Abstract

The present invention relates to polynucleotide and polypeptide molecules for zFGF-5, a novel member of the FGF family. The polypeptides, and polynucleotides encoding them, are proliferative for muscle cells and may be used for remodelling cardiac tissue and improving cardiac function. The present invention also includes antibodies to the zFGF-5 polypeptides.

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FIBROBLAST GROWTH FACTOR HOMOLOGS

REFERENCE TO RELATED APPLICATIONS

This application is related to Provisional Application 60/028,646, filed on October 16, 1996. Under 35 U.S.C. § 119(e)(1), this application claims benefit of said Provisional Application.

BACKGROUND OF THE INVENTION

The fibroblast growth factor (FGF) family consists of at least nine distinct members (Basilico et al., Adv. Cancer Res. 59:115-165, 1992 and Fernig et al., Prog. Growth Factor Res. 5(4):353-377, 1994) which generally act as mitogens for a broad spectrum of cell types. For example, basic FGF (also known as FGF-2) is mitogenic *in vitro* for endothelial cells, vascular smooth muscle cells, fibroblasts, and generally for cells of mesoderm or neuroectoderm origin, including cardiac and skeletal myocytes (Gospodarowicz et al., J. Cell. Biol. 70:395-405, 1976; Gospodarowicz et al., J. Cell. Biol. 89:568-578, 1981 and Kardami, J. Mol. Cell. Biochem. 92:124-134, 1990). *In vivo*, bFGF has been shown to play a role in avian cardiac development (Sugi et al., Dev. Biol. 168:567-574, 1995 and Mima et al., Proc. Nat'l. Acad. Sci. 92:467-471, 1995), and to induce coronary collateral development in dogs (Lazarous et al., Circulation 94:1074-1082, 1996). In addition, non-mitogenic activities have been demonstrated for various members of the FGF family. Non-proliferative activities associated with acidic and/or basic FGF include: increased endothelial release of tissue plasminogen activator, stimulation of extracellular matrix synthesis, chemotaxis for endothelial cells, induced expression of fetal contractile genes in cardiomyocytes

(Parker et al., J. Clin. Invest. 85:507-514, 1990), and enhanced pituitary hormonal responsiveness (Baird et al. J. Cellular Physiol. 5:101-106, 1987.)

Several members of the FGF family do not have a signal sequence (aFGF, bFGF and possibly FGF-9) and thus would not be expected to be secreted. In addition, several of the FGF family members have the ability to migrate to the cell nucleus (Friesel et al., FASEB 9:919-925, 1995). All the members of the FGF family bind heparin based on structural similarities. Structural homology crosses species, suggesting a conservation of their structure/function relationship (Ornitz et al., J. Biol. Chem. 271(25):15292-15297, 1996.)

There are four known extracellular FGF receptors (FGFRs), and they are all tyrosine kinases. In general, the FGF family members bind to all of the known FGFRs, however, specific FGFs bind to specific receptors with higher degrees of affinity. Another means for specificity within the FGF family is the spatial and tempora: expression of the ligands and their receptors during embryogenesis. Evidence suggests that the FGFs most likely act only in autocrine and/or paracrine manner, due to their heparin binding affinity, which limits their diffusion from the site of release (Flaumenhaft et al., J. Cell. Biol. 111(4):1651-1659, 1990.) Basic FGF lacks a signal sequence, and is therefore restricted to paracrine or autocrine modes of action. It has been postulated that basic FGF is stored intracellularly and released upon tissue damage. Basic FGF has been shown to have two receptor binding regions that are distinct from the heparin binding site (Abraham et al.,. EMBO J. 5(10):2523-2528, 1986.)

It has been shown that FGFR-3 plays a role in bone growth. Mice made homozygous null for the FGFR-3 (-/-) resulted in postnatal skeletal abnormalities (Colvin et al., Nature Genet. 12:309-397, 1996 and Deng et al.,

Cell 84:911-921, 1996). The mutant phenotype suggests that in normal mice, FGFR-3 plays a role in regulation of chrondrocyte cell division in the growth plate region of the bone (Goldfarb, Cytokine and Growth Factor Rev. 7(4):311-325, 1996). The ligand for the FGFR-3 in the bone growth plate has not been identified.

Although four FGFRs have been identified, all of which have been shown to have functional splice variants, the possibility that novel FGF receptors exist is quite likely. For example, no receptor has been identified for the FGF-8a isoform (MacArthur et al., J. Virol. 69(4):2501-2507, 1995.).

FGF-8 is a member of the FGF family that was originally isolated from mammary carcinoma cells as an androgen-inducible mitogen. It has been mapped to human chromosome 10q25-q26 (White et al., Genomics 30:109-11, 1995.) FGF-8 is involved in embryonic limb development (Vogel et al., Development 122:1737-1750, 1996 and Tanaka et al., Current Biology 5(6):594-597, 1995.) Expression of FGF-8 during embryogenesis in cardiac, urogenital and neural tissue indicates that it may play a role in development of these tissues (Crossley et al., Development 121:439-451, 1995.) There is some evidence that acrocephalosyndactylia, a congenital condition marked by peaked head and webbed fingers and toes, is associated with FGF-8 point mutations (White et al., 1995, ibid.)

FGF-8 has five exons, in contrast to the other known FGFs, which have only three exons. The first three exons of FGF-8 correspond to the first exon of the other FGFs (MacArthur et al., Development 121:3603-3613, 1995.) The human gene for FGF-8 codes for four isoforms which differ in their N-terminal regions: FGF isoforms a, b, e, and f; in contrast to the murine gene which gives rise to eight FGF-8 isoforms (Crossley et al., 1995, ibid.) Human FGF-8a and FGF-8b have 100% homology to the murine proteins, and FGF-8e and FGF-8f proteins are 98%

homologous between human and mouse (Gemel et al., Genomics 35:253-257, 1996.)

Heart disease is the major cause of death in the United States, accounting for up to 30% of all deaths. Myocardial infarction (MI) accounts for 750,000 hospital admissions per year in the U.S., with more than 5 million people diagnosed with coronary disease. Risk factors for MI include diabetes mellitus, hypertension, truncal obesity, smoking, high levels of low density lipoprotein in the plasma or genetic predisposition.

Cardiac hyperplasia is an increase in cardiac myocyte proliferation, and has been demonstrated to occur with normal aging in the human and rat (Olivetti et al., J. Am. Coll. Cardiol. 24(1):140-9, 1994 and Anversa et al., Circ. Res. 67:871-885, 1990), and in catecholamine-induced cardiomyopathy in rats (Deisher et al., Am. J. Cardiovasc. Pathol. 5(1):79-88, 1994.) Whether the increase in myocytes originate with some progenitor, or are a result of proliferation of a more terminally differentiated cell type, remains controversial.

However, because infarction and other causes of myocardial necrosis appear to be irreparable, it appears that the normal mechanisms of cardiac hyperplasia cannot compensate for extensive myocyte death and there remains a need for exogenous factors that promote hyperplasia and ultimately result in renewal of the heart's ability to function.

Bone remodeling is the dynamic process by which tissue mass and skeletal architecture are maintained. The process is a balance between bone resorption and bone formation, with two cell types thought to be the major players. These cells are the osteoblast and osteoclast. Osteoblasts synthesize and deposit matrix to become new bone. The activities of osteoblasts and osteoclasts are regulated by many factors, systemic and local, including growth factors.

While the interaction between local and systemic factors has not been completely elucidated, there does appear to be consensus that growth factors play a key role in the regulation of both normal skeletal remodeling and fracture repair.. Some of the growth factors that have been identified in bone include: IGF-I, IGF-II, TGF-β_1, TGF-β_2, bFGF, aFGF, PDGF and the family of bone morphogenic proteins (Baylink et al., J. Bone Mineral Res. 8 (Supp. 2):S565-S572, 1993).

When bone resorption exceeds bone formation, a net loss in bone results, and the propensity for fractures is increased. Decreased bone formation is associated with aging and certain pathological states. In the U.S. alone, there are approximately 1.5 million fractures annually that are attributed to osteoporosis. The impact of these fractures on the quality of the patient's life is immense. Associated costs to the health care system in the U.S. are estimated to be $5-$10 billion annually, excluding long-term care costs.

Other therapeutic applications for growth factors influencing bone remodeling include, for example, the treatment of injuries which require the proliferation of osteoblasts to heal, such as fractures, as well as stimulation of mesenchymal cell proliferation and the synthesis of intramembraneous bone which have been indicated as aspects of fracture repair (Joyce et al. 36th Annual Meeting, Orthopaedic Research Society, February 5-8, 1990. New Orleans, LA).

The present invention provides such polypeptides for these and other uses that should be apparent to those skilled in the art from the teachings herein.

SUMMARY OF THE INVENTION

Within one aspect, the present invention provides An isolated polynucleotide molecule encoding a fibroblast growth factor (FGF) homolog polypeptide

selected from the group consisting of: a) polynucleotide molecules comprising a nucleotide sequence as shown in SEQ ID NO: 1 from nucleotide 82 to nucleotide 621; b) allelic variants of (a); c) polynucleotide molecules that encode a polypeptide that is at least 60% identical to the amino acid sequence of SEQ ID NO: 2 from amino acid residue 28 (Glu) to amino acid residue 207 (Ala); and d) polynucleotide molecules comprising a nucleotide sequence as shown in SEQ ID NO: 6 from nucleotide 82 to nucleotide 621.

In one embodiment, the isolated polynucleotide molecule comprises a nucleotide sequence as shown in SEQ ID NO: 1 from nucleotide 1 to nucleotide 621 or a nucleotide sequence as shown in SEQ ID NO: 6 from nucleotide 1 to nucleotide 621.

In another embodiment, the isolated polynucleotide molecule comprises a nucleotide sequence as shown in SEQ ID NO: 1 from nucleotide 82 to nucleotide 621.

In another aspect, the present invention provides an expression vector comprising the following operably linked elements: a transcription promoter; a DNA segment selected from the group consisting of: a) polynucleotide molecules comprising a nucleotide sequence as shown in SEQ ID NO: 1 from nucleotide 82 to nucleotide 621; b) allelic variants of (a); c) polynucleotide molecules that encode a polypeptide that is at least 60% identical to the amino acid sequence of SEQ ID NO: 2 from amino acid residue 28 (Glu) to amino acid residue 207 (Ala); and d) polynucleotide molecules comprising a nucleotide sequence as shown in SEQ ID NO: 6 from nucleotide 82 to nucleotide 621; and a transcription terminator.

In another aspect, the present invention provides a cultured cell into which has been introduced an expression vector comprising the following operably linked

elements: a transcription promoter; a DNA segment selected from the group consisting of: a) polynucleotide molecules comprising a nucleotide sequence as shown in SEQ ID NO: 1 from nucleotide 82 to nucleotide 621; b) allelic variants of (a); c) polynucleotide molecules that encode a polypeptide that is at least 60% identical to the amino acid sequence of SEQ ID NO: 2 from amino acid residue 28 (Glu) to amino acid residue 207 (Ala); and d) polynucleotide molecules comprising a nucleotide sequence as shown in SEQ ID NO: 6 from nucleotide 82 to nucleotide 621; and a transcription terminator, wherein said cell expresses a polypeptide encoded by the DNA segment.

In another aspect, the present invention provides a method of producing an FGF homolog polypeptide comprising: culturing a cell into which has been introduced an expression vector comprising the following operably linked elements: a transcription promoter; a DNA segment selected from the group consisting of: a) polynucleotide molecules comprising a nucleotide sequence as shown in SEQ ID NO: 1 from nucleotide 82 to nucleotide 621; b) allelic variants of (a); c) polynucleotide molecules that encode a polypeptide that is at least 60% identical to the amino acid sequence of SEQ ID NO: 2 from amino acid residue 28 (Glu) to amino acid residue 207 (Ala); and d) polynucleotide molecules comprising a nucleotide sequence as shown in SEQ ID NO: 6 from nucleotide 82 to nucleotide 621; and a transcription terminator, whereby said cell expresses a FGF homolog polypeptide encoded by the DNA segment; and recovering the FGF homolog polypeptide.

In another aspect, the present invention provides an isolated FGF homolog polypeptide selected from the group consisting of: a) polypeptide molecules comprising an amino acid sequence as shown in SEQ ID NO: 2 from residue 28 (Glu) to residue 175 (Met); b) allelic variants of (a); and c) polypeptide molecules that are at

least 60% identical to SEQ ID NO: 2 from amino acid residue 28 (Glu) to amino acid residue 175 (Met).

In another aspect, the present invention provides an isolated FGF homolog polypeptide selected from the group consisting of: a) polypeptide molecules comprising an amino acid sequence as shown in SEQ ID NO: 2 from residue 28 (Glu) to residue 196 (Lys); b) allelic variants of (a); and c) polypeptide molecules that are at least 60% identical to SEQ ID NO: 2 from amino acid residue 28 (Glu) to amino acid residue 196 (Lys).

In another embodiment, the present invention provides an isolated FGF homolog polypeptide selected from the group consisting of: a) polypeptide molecules comprising an amino acid sequence as shown in SEQ ID NO: 2 from residue 28 (Glu) to residue 207 (Ala); b) allelic variants of (a); and c) polypeptide molecules that are at least 60% identical to the amino acids of SEQ ID NO: 2 from amino acid residue 28 (Glu) to amino acid residue 207 (Ala).

In an additional embodiment, the present invention provides an FGF homolog polypeptide further comprising a signal sequence.

In another embodiment, the present invention provides an FGF homolog polypeptide further comprising a signal sequence as shown in SEQ ID NO: 2 from amino acid residue 1 (Met) to amino acid residue 27 (Ala).

The present invention also provides pharmaceutical composition comprising a purified FGF homolog polypeptide, in combination with a pharmaceutically acceptable vehicle.

In another aspect, the present invention provides an antibody that binds to an epitope of a polypeptide molecule comprising an amino acid sequence as shown in SEQ ID NO: 2 from residue 1 (Met) to residue 207 (Ala).

In another embodiment, the present invention provides an antibody that binds a polypeptide molecule comprising an amino acid sequence as shown in SEQ ID NO: 2 from residue 28 (Glu) to residue 196 (Lys).

In another aspect, the present invention provides a method of stimulating proliferation of myocytes or myocyte progenitors comprising administering to a mammal in need thereof, an amount of an FGF homolog polypeptide sufficient to produce a clinically significant increase in the number of myocytes or myocyte progenitors in said mammal.

In another embodiment, the present invention provides a method of stimulating proliferation of myocytes or myocyte progenitors, wherein the myocytes or myocyte progenitors are cardiac myocytes or cardiac myocytes progenitors.

In another aspect, the present invention provides a method for *ex vivo* stimulation of myocyte progenitor cells or myocytes comprising culturing heart tissue cells with an amount of an FGF homolog polypeptide sufficient to produce an increase in the number of myocyte progenitor cells or myocytes in the heart tissue cells cultured in the presence of an FGF homolog polypeptide, as compared to heart tissue myocyte progenitor cells or myocytes cultured in the absence of an FGF homolog polypeptide.

In another embodiment, the present invention provides a method for *ex vivo* stimulation of myocyte progenitor cells or myocytes, wherein the myocytes or myocyte progenitors are cardiac myocytes or cardiac myocytes progenitors.

In another aspect, the present invention provides a method of delivering an agent or drug selectively to heart tissue comprising: linking a first molecule comprising an FGF homolog polypeptide with a

second molecule comprising an agent or drug to form a chimera; and administering the chimera to heart tissue.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 and Figure 2 illustrate a multiple alignment of human fibroblast growth factor homologous factor 1 (FHF-1), human myocyte-activating factor (FGF-10), human fibroblast growth factor homologous factor 4 (FHF-4), human fibroblast growth factor homologous factor 2 (FHF-2), human fibroblast growth factor homologous factor 3 (FHF-3), human FGF-4, human FGF-6, human FGF-2 (basic), human FGF-1 (acidic), human keratinocyte growth factor 2 (KGF-2), human keratinocyte growth factor precursor (FGF-7), human zFGF-5, human FGF-8, human FGF-5, human FGF-9, and human FGF-3. "*" designates conserved amino acids; ":" designates conserved amino acid substitutions; and "." designates less stringently conserved amino acid substitutions.

Figure 3 is an inter-family similarity matrix illustrating the percent identity between human FGF-5, human FGF-6, human FGF-7, human FGF-8, human FGF-9, human zFGF-5, human FGF-10, human FGF-1, human FHF-1, human FGF-2, human FHF-2, human FHF-4, human FGF-3, human KGF-2, human FHF-3, and human FGF-4.

DETAILED DESCRIPTION OF THE INVENTION

The term "ortholog" (or "species homolog") denotes a polypeptide or protein obtained from one species that has homology to an analogous polypeptide or protein from a different species.

The term "paralog" denotes a polypeptide or protein obtained from a given species that has homology to a distinct polypeptide or protein from that same species.

The term "allelic variant" denotes any of two or more alternative forms of a gene occupying the same chromosomal locus. Allelic variation arises naturally

through mutation, and may result in phenotypic polymorphism within populations. Gene mutations can be silent (no change in the encoded polypeptide) or may encode polypeptides having altered amino acid sequence. The term allelic variant is also used herein to denote a protein encoded by an allelic variant of a gene.

The term "expression vector" denotes a DNA molecule, linear or circular, that comprises a segment encoding a polypeptide of interest operably linked to additional segments that provide for its transcription. Such additional segments may include promoter and terminator sequences, and may optionally include one or more origins of replication, one or more selectable markers, an enhancer, a polyadenylation signal, and the like. Expression vectors are generally derived from plasmid or viral DNA, or may contain elements of both.

The term "isolated", when applied to a polynucleotide molecule, denotes that the polynucleotide has been removed from its natural genetic milieu and is thus free of other extraneous or unwanted coding sequences, and is in a form suitable for use within genetically engineered protein production systems. Such isolated molecules are those that are separated from their natural environment and include cDNA and genomic clones. Isolated DNA molecules of the present invention are free of other genes with which they are ordinarily associated, but may include naturally occurring 5' and 3' untranslated regions such as promoters and terminators. The identification of associated regions will be evident to one of ordinary skill in the art (see for example, Dynan and Tijan, Nature 316:774-78, 1985). When applied to a protein, the term "isolated" indicates that the protein is found in a condition other than its native environment, such as apart from blood and animal tissue. In a preferred form, the isolated protein is substantially free of other proteins, particularly other proteins of animal

origin. It is preferred to provide the protein in a highly purified form, i.e., greater than 95% pure, more preferably greater than 99% pure.

The term "operably linked", when referring to DNA segments, denotes that the segments are arranged so that they function in concert for their intended purposes, e.g. transcription initiates in the promoter and proceeds through the coding segment to the terminator

The term "polynucleotide" denotes a single- or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases read from the 5' to the 3' end. Polynucleotides include RNA and DNA, and may be isolated from natural sources, synthesized *in vitro*, or prepared from a combination of natural and synthetic molecules.

The term "complements of polynucleotide molecules" denotes polynucleotide molecules having a complementary base sequence and reverse orientation as compared to a reference sequence. For example, the sequence 5' ATGCACGGG 3' is complementary to 5' CCCGTGCAT 3'.

The term "degenerate nucleotide sequence" denotes a sequence of nucleotides that includes one or more degenerate codons (as compared to a reference polynucleotide molecule that encodes a polypeptide). Degenerate codons contain different triplets of nucleotides, but encode the same amino acid residue (i.e., GAU and GAC triplets each encode Asp).

The term "promoter" denotes a portion of a gene containing DNA sequences that provide for the binding of RNA polymerase and initiation of transcription. Promoter sequences are commonly, but not always, found in the 5' non-coding regions of genes.

The term "secretory signal sequence" denotes a DNA sequence that encodes a polypeptide (a "secretory peptide") that, as a component of a larger polypeptide, directs the larger polypeptide through a secretory pathway

of a cell in which it is synthesized. The larger peptide is commonly cleaved to remove the secretory peptide during transit through the secretory pathway.

The term "receptor" denotes a cell-associated protein that binds to a bioactive molecule (i.e., a ligand) and mediates the effect of the ligand on the cell. Membrane-bound receptors are characterized by a multi-domain structure comprising an extracellular ligand-binding domain and an intracellular effector domain that is typically involved in signal transduction. Binding of ligand to receptor results in a conformational change in the receptor that causes an interaction between the effector domain and other molecule(s) in the cell. This interaction in turn leads to an alteration in the metabolism of the cell. Metabolic events that are linked to receptor-ligand interactions include gene transcription, phosphorylation, dephosphorylation, increases in cyclic AMP production, mobilization of cellular calcium, mobilization of membrane lipids, cell adhesion, hydrolysis of inositol lipids and hydrolysis of phospholipids. Most nuclear receptors also exhibit a multi-domain structure, including an amino-terminal, transactivating domain, a DNA binding domain and a ligand binding domain. In general, receptors can be membrane bound, cytosolic or nuclear; monomeric (e.g., thyroid stimulating hormone receptor, beta-adrenergic receptor) or multimeric (e.g., PDGF receptor, growth hormone receptor, IL-3 receptor, GM-CSF receptor, G-CSF receptor, erythropoietin receptor and IL-6 receptor).

The term "complement/anti-complement pair" denotes non-identical moieties that form a non-covalently associated, stable pair under appropriate conditions. For instance, biotin and avidin (or streptavidin) are prototypical members of a complement/anti-complement pair. Other exemplary complement/anti-complement pairs include receptor/ligand pairs, antibody/antigen (or hapten or

epitope) pairs, sense/antisense polynucleotide pairs, and the like. Where subsequent dissociation of the complement/anti-complement pair is desirable, the complement/anti-complement pair preferably has a binding affinity of $<10^9\ M^{-1}$.

The present invention is based in part upon the discovery of a novel DNA sequence that encodes a fibroblast growth factor (FGF) homolog polypeptide having homology to FGF-8. Analysis of the tissue distribution of the mRNA corresponding to this novel DNA showed that expression was highest in fetal heart tissue and adult heart tissue, followed by apparent but decreased expression levels in fetal lung, skeletal muscle, smooth muscle tissues such as small intestine, colon and trachea. The FGF homolog polypeptide has been designated zFGF-5.

The novel zFGF-5 polypeptides of the present invention were initially identified by querying an EST database for growth factors. A single EST sequence was discovered and predicted to be related to the FGF family. The novel FGF homolog polypeptide encoded by the full length cDNA contained a motif of the formula: CXFXEX{6}Y, wherein X is any amino acid and X{} is the number of X amino acids greater than one. This motif occurs in all known members of the FGF family and is unique to these proteins.

The nucleotide sequence of the zFGF-5 cDNA is described in SEQ ID NO. 1, and its deduced amino acid sequence is described in SEQ ID NO. 2. When amino acid residue 28 (Glu) to amino acid residue 181 (Gln) of SEQ ID NO: 2 is compared to the corresponding region of FGF-8 (See Figures 1 and 2) the aligned and deduced amino acid sequence has approximately 56% identity.

The novel polypeptide encoded by the polynucleotide described herein contains the CXFXE{6}Y motif present in all members of the FGF family. The CXFXE{6}Y motifs are highly conserved. A consensus amino

acid sequence of the CXFXEX{6}Y domain includes human fibroblast growth factor homologous factor 1 (FHF-1; Smallwood et al., Proc. Natl. Acad. Sci. USA 93:9850-9857, 1996), human myocyte-activating factor (FGF-10; HSU76381, GENBANK identifier, http://www.ncbi.nlm.nih.gov/), human fibroblast growth factor homologous factor 4 (FHF-4; Smallwood et al., 1996, *ibid.*), human fibroblast growth factor homologous factor 2 (FHF-2; Smallwood et al., 1996, *ibid.*), human fibroblast growth factor homologous factor 3 (FHF-3; Smallwood et al., 1996, *ibid.*), human FGF-4 (Basilico et al., Adv. Cancer Res. 59:115-165,1992), human FGF-6 (Basilico et al., 1992, *ibid.*), human FGF-2 (basic; Basilico et al., 1992, *ibid.*), human FGF-1 (acidic; Basilico et al., 1992, *ibid.*), human keratinocyte growth factor 2 (KGF-2; HSU67918 GENBANK identifier, http://www.ncbi.nlm.nih.gov/), human keratinocyte growth factor precursor (FGF-7; Basilico et al., 1992, *ibid.*), human zFGF-5, human FGF-8 (Gemel et al., Genomics 35:253-257, 1996), human FGF-5 (Basilico et al., 1992, *ibid.*), human FGF-9 (Miyamoto et al., Mol. Cell. Biol. 13:4251-4259, 1993), and human FGF-3 (Basilico et al., 1992, *ibid.*)

Analysis of the cDNA encoding a zFGF-5 polypeptide (SEQ ID NO: 1) revealed an open reading frame encoding 207 amino acids (SEQ ID NO: 2) comprising a mature polypeptide of 180 amino acids (residue 28 to residue 207 of SEQ ID NO: 2). Multiple alignment of zFGF-5 with other known FGFs revealed a block of high percent identity corresponding to amino acid residue 127 (Cys) to amino acid residue 138 (Tyr), of SEQ ID NO: 2 and is shown in the Figure. Several of the members of the FGF family do not have signal sequences.

Members of the FGF family are characterized by heparin binding domains. A putative heparin-binding domain for zFGF-5 has been identified in the region of amino acid residue 148 (Gly) to amino acid residue 169

(Gln) of SEQ ID NO: 2. It is postulated that receptor-mediated signaling is initiated upon binding of FGF ligand complexed with cell-surface heparin sulfate proteoglycans. Many FGF family members can be placed into one of two related families on the basis of their structures and functions. aFGF and bFGF consist of three exons separated by two introns of variable length. FGF-8 consists of five exons, the first three of which correspond to the first exon of aFGF and bFGF. All the known FGF family members are spliced to form single polypeptides.

SEQ ID NO: 6 is a degenerate polynucleotide sequence that encompasses all polynucleotides that could encode the zFGF-5 polypeptide of SEQ ID NO: 2 (amino acids 1 or 28 to 207). Thus, zFGF-5 polypeptide-encoding polynucleotides ranging from nucleotide 1 or 82 to nucleotide 621 of SEQ ID NO: 6 are contemplated by the present invention. Also contemplated by the present invention are fragments and fusions as described above with respect to SEQ ID NO: 1, which are formed from analogous regions of SEQ ID NO: 6, wherein nucleotides 82 to 621 of SEQ ID NO: 6 correspond to nucleotides 82 to 621 of SEQ ID NO: 1, for the encoding a mature zFGF-5 molecule.

The symbols in SEQ ID NO: 6 are summarized in Table 1 below.

TABLE 1

Nucleotide	Resolutions	Complement	Resolutions
A	A	T	T
C	C	G	G
G	G	C	C
T	T	A	A
R	A|G	Y	C|T
Y	C|T	R	A|G
M	A|C	K	G|T
K	G|T	M	A|C
S	C|G	S	C|G
C|G	A|T	W	A|T
H	A|C|T	D	A|G|T
B	C|G|T	V	A|C|G
V	A|C|G	B	C|G|T
D	A|G|T	H	A|C|T
N	A|C|G|T	N	A|C|G|T

The degenerate codons used in SEQ ID NO: 6, encompassing all possible codons for a given amino acid, are set forth in Table 2 below.

TABLE 2

Amino Acid	Letter	Codons	Degenerate Codon
Cys	C	TGC TGT	TGY
Ser	S	AGC AGT TCA TCC TCG TCT	WSN
Thr	T	ACA ACC ACG ACT	ACN
Pro	P	CCA CCC CCG CCT	CCN
Ala	A	GCA GCC GCG GCT	GCN
Gly	G	GGA GGC GGG GGT	GGN
Asn	N	AAC AAT	AAY
Asp	D	GAC GAT	GAY
Glu	E	GAA GAG	GAR
Gln	Q	CAA CAG	CAR
His	H	CAC CAT	CAY
Arg	R	AGA AGG CGA CGC CGG CGT	MGN
Lys	K	AAA AAG	AAR
Met	M	ATG	ATG
Ile	I	ATA ATC ATT	ATH
Leu	L	CTA CTC CTG CTT TTA TTG	YTN
Val	V	GTA GTC GTG GTT	GTN
Phe	F	TTC TTT	TTY
Tyr	Y	TAC TAT	TAY
Trp	W	TGG	TGG
Ter	.	TAA TAG TGA	TRR
Asn|Asp	B		RAY
Glu|Gln	Z		SAR
Any	X		NNN
Gap	-	---	

One of ordinary skill in the art will appreciate that some ambiguity is introduced in determining a degenerate codon, representative of all possible codons encoding each amino acid. For example, the degenerate codon for serine (WSN) can, in some circumstances, encode arginine (AGR), and the degenerate codon for arginine

(MGN) can, in some circumstances, encode serine (AGY). A similar relationship exists between codons encoding phenylalanine and leucine. Thus, some polynucleotides encompassed by the degenerate sequence may have some incorrect amino acids, but one of ordinary skill in the art can easily identify such erroneous sequences by reference to the amino acid sequence of SEQ ID NO: 2.

The highly conserved amino acids in zFGF-5 can be used as a tool to identify new family members. To identify new family members in EST databases, the conserved CXFXEX{6}Y motif can be used. In another method using polynucleotide probes and hybridization methods, RNA obtained from a variety of tissue sources can be used to generate cDNA libraries and probe these libraries for new family members. In particular, reverse transcription-polymerase chain reaction (RT-PCR) can be used to amplify sequences encoding highly degenerate DNA primers designed from the sequences corresponding to amino acid residue 127 (Cys) to amino acid residue 138 (Tyr) of SEQ ID NO: 2.

Within preferred embodiments of the invention the isolated polynucleotides will serve as a probe and hybridize to similar sized regions of SEQ ID NO: 1 or a sequence complementary thereto, under stringent conditions. In general, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Typical stringent conditions are those in which the salt concentration is at least about 0.02 M at pH 7 and the temperature is at least about 60°C.

As previously noted, the isolated polynucleotides of the present invention include DNA and RNA. Methods for isolating DNA and RNA are well known in the art. It is generally preferred to isolate RNA from

cardiac tissue, although DNA can also be prepared using RNA from other tissues or isolated as genomic DNA. Total RNA can be prepared using guanidine HCl extraction followed by isolation by centrifugation in a CsCl gradient (Chirgwin et al., Biochemistry 18:52-94, 1979). Poly $(A)^+$ RNA is prepared from total RNA using the method of Aviv and Leder (Proc. Natl. Acad. Sci. USA 69:1408-1412, 1972). Complementary DNA (cDNA) is prepared from poly$(A)^+$ RNA using known methods. Polynucleotides encoding zFGF-5 polypeptides are then identified and isolated by, for example, hybridization or PCR.

The present invention further provides counterpart polypeptides and polynucleotides from other species (orthologs or paralogs). Of particular interest are zFGF-5 polypeptides from other mammalian species, including murine, rat, porcine, ovine, bovine, canine, feline, equine and other primate proteins. Identification of paralogs of the human sequence are particularly interesting because while 8 paralogs of murine FGF-8 have been identifed, only 4 human paralogs are known. Human paralogs or species homologs of the human proteins can be cloned using information and compositions provided by the present invention in combination with conventional cloning techniques. For example, a cDNA can be cloned using mRNA obtained from a tissue or cell type that expresses the protein. Suitable sources of mRNA can be identified by probing Northern blots with probes designed from the sequences disclosed herein. A library is then prepared from mRNA of a positive tissue or cell line. A zFGF-5-encoding cDNA can then be isolated by a variety of methods, such as by probing with a complete or partial human cDNA or with one or more sets of degenerate probes based on the disclosed sequences. A cDNA can also be cloned using the polymerase chain reaction, or PCR (Mullis, U.S. Patent 4,683,202), using primers designed from the sequences disclosed herein. Within an additional

method, the cDNA library can be used to transform or transfect host cells, and expression of the cDNA of interest can be detected with an antibody to zFGF-5. Similar techniques can also be applied to the isolation of genomic clones.

Those skilled in the art will recognize that the sequences disclosed in SEQ ID NO: 1 and SEQ ID NO: 2 represent a single allele of the human zFGF-5 gene and polypeptide, and that allelic variation and alternative splicing are expected to occur. Allelic variants can be cloned by probing cDNA or genomic libraries from different individuals according to standard procedures. Allelic variants of the DNA sequence shown in SEQ ID NO: 1, including those containing silent mutations and those in which mutations result in amino acid sequence changes, are within the scope of the present invention, as are proteins which are allelic variants of SEQ ID NO: 2.

The present invention also provides isolated zFGF-5 polypeptides that are substantially homologous to the polypeptides of SEQ ID NO: 2 and their species homologs/ orthologs. The term "substantially homologous" is used herein to denote polypeptides having 50%, preferably 60%, more preferably at least 80%, sequence identity to the sequences shown in SEQ ID NO: 2 or their orthologs or paralogs. Such polypeptides will more preferably be at least 90% identical, and most preferably 95% or more identical to SEQ ID NO: 2 or its orthologs or paralogs. Percent sequence identity is determined by conventional methods. See, for example, Altschul et al., Bull. Math. Bio. 48: 603-616, 1986 and Henikoff and Henikoff, Proc. Natl. Acad. Sci. USA 89:10915-10919, 1992. Briefly, two amino acid sequences are aligned to optimize the alignment scores using a gap opening penalty of 10, a gap extension penalty of 1, and the "blosum 62" scoring matrix of Henikoff and Henikoff (ibid.) as shown in Table

3 (amino acids are indicated by the standard one-letter codes). The percent identity is then calculated as:

Table 3

	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
A	4																			
R	-1	5																		
N	-2	0	6																	
D	-2	-2	1	6																
C	0	-3	-3	-3	9															
Q	-1	1	0	0	-3	5														
E	-1	0	0	2	-4	2	5													
G	0	-2	0	-1	-3	-2	-2	6												
H	-2	0	1	-1	-3	0	0	-2	8											
I	-1	-3	-3	-3	-1	-3	-3	-4	-3	4										
L	-1	-2	-3	-4	-1	-2	-3	-4	-3	2	4									
K	-1	2	0	-1	-3	1	1	-2	-1	-3	-2	5								
M	-1	-1	-2	-3	-1	0	-2	-3	-2	1	2	-1	5							
F	-2	-3	-3	-3	-2	-3	-3	-3	-1	0	0	-3	0	6						
P	-1	-2	-2	-1	-3	-1	-1	-2	-2	-3	-3	-1	-2	-4	7					
S	1	-1	1	0	-1	0	0	0	-1	-2	-2	0	-1	-2	-1	4				
T	0	-1	0	-1	-1	-1	-1	-2	-2	-1	-1	-1	-1	-2	-1	1	5			
W	-3	-3	-4	-4	-2	-2	-3	-2	-2	-3	-2	-3	-1	1	-4	-3	-2	11		
Y	-2	-2	-2	-3	-2	-1	-2	-3	2	-1	-1	-2	-1	3	-3	-2	-2	2	7	
V	0	-3	-3	-3	-1	-2	-2	-3	-3	3	1	-2	1	-1	-2	-2	0	-3	-1	4

$$\frac{\text{Total number of identical matches}}{\text{[length of the longer sequence plus the number of gaps introduced into the longer sequence in order to align the two sequences]}} \times 100$$

Sequence identity of polynucleotide molecules is determined by similar methods using a ratio as disclosed above.

Substantially homologous proteins and polypeptides are characterized as having one or more amino acid substitutions, deletions or additions. These changes are preferably of a minor nature, that is conservative amino acid substitutions (see Table 4) and other substitutions that do not significantly affect the folding or activity of the protein or polypeptide; small deletions, typically of one to about 30 amino acids; and small amino- or carboxyl-terminal extensions, such as an amino-terminal methionine residue, a small linker peptide of up to about 20-25 residues, or a small extension that facilitates purification (an affinity tag), such as a poly-histidine tract, protein A (Nilsson et al., EMBO J. 4:1075, 1985; Nilsson et al., Methods Enzymol. 198:3, 1991), glutathione S transferase (Smith and Johnson, Gene 67:31, 1988), maltose binding protein (Kellerman and Ferenci, Methods Enzymol. 90:459-463, 1982; Guan et al., Gene 67:21-30, 1987), or other antigenic epitope or binding domain. See, in general Ford et al., Protein Expression and Purification 2: 95-107, 1991, which is incorporated herein by reference. DNAs encoding affinity tags are available from commercial suppliers (e.g., Pharmacia Biotech, Piscataway, NJ; New England Biolabs, Beverly, MA).

Table 4

Conservative amino acid substitutions

Basic:	arginine
	lysine
	histidine
Acidic:	glutamic acid
	aspartic acid
Polar:	glutamine
	asparagine
Hydrophobic:	leucine
	isoleucine
	valine
Aromatic:	phenylalanine
	tryptophan
	tyrosine
Small:	glycine
	alanine
	serine
	threonine
	methionine

The proteins of the present invention can also comprise, in addition to the 20 standard amino acids, non-naturally occurring amino acid residues. Non-naturally occurring amino acids include, without limitation, trans-3-methylproline, 2,4-methanoproline, cis-4-hydroxyproline, trans-4-hydroxyproline, N-methyl-glycine, allo-threonine, methylthreonine, hydroxyethyl-cysteine, hydroxyethylhomocysteine, nitroglutamine, homoglutamine, pipecolic acid, tert-leucine, norvaline, 2-azaphenylalanine, 3-azaphenylalanine, 4-azaphenyl-alanine, 4-fluorophenylalanine, 4-hydroxyproline, 6-*N*-methyl lysine, 2-aminoisobutyric acid, isovaline and α-methyl serine. Several methods are known in the art for incorporating non-naturally occurring amino acid residues into proteins. For example, an *in vitro* system can be

employed wherein nonsense mutations are suppressed using chemically aminoacylated suppressor tRNAs. Methods for synthesizing amino acids and aminoacylating tRNA are known in the art. Transcription and translation of plasmids containing nonsense mutations are carried out in a cell free system comprising an *E. coli* S30 extract and commercially available enzymes and other reagents. Proteins are purified by chromatography. See, for example, Robertson et al., J. Am. Chem. Soc. 113:2722, 1991; Ellman et al., Meth. Enzymol. 202:301, 1991; Chung et al., Science 259:806-09, 1993; and Chung et al., Proc. Natl. Acad. Sci. USA 90:10145-49, 1993). In a second method, translation is carried out in *Xenopus* oocytes by microinjection of mutated mRNA and chemically aminoacylated suppressor tRNAs (Turcatti et al., J. Biol. Chem. 271:19991-98, 1996). Within a third method, *E. coli* cells are cultured in the absence of a natural amino acid that is to be replaced (e.g., phenylalanine) and in the presence of the desired non-naturally occurring amino acid(s) (e.g., 2-azaphenylalanine, 3-azaphenylalanine, 4-azaphenylalanine, or 4-fluorophenylalanine). The non-naturally occurring amino acid is incorporated into the protein in place of its natural counterpart. See, Koide et al., Biochem. 33:7470-76, 1994. Naturally occurring amino acid residues can be converted to non-naturally occurring species by *in vitro* chemical modification. Chemical modification can be combined with site-directed mutagenesis to further expand the range of substitutions (Wynn and Richards, Protein Sci. 2:395-403, 1993).

Essential amino acids in the zFGF-5 polypeptides of the present invention can be identified according to procedures known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham and Wells, Science 244: 1081-1085, 1989). In the latter technique, single alanine mutations are introduced at every residue in the molecule, and the resultant mutant

molecules are tested for biological activity (e.g., proliferation of cardiac myocytes or fibroblasts, or stimulation of bone formation) to identify amino acid residues that are critical to the activity of the molecule. See also, Hilton et al., J. Biol. Chem. 271:4699-4708, 1996. Sites of ligand-receptor interaction can also be determined by physical analysis of structure, as determined by such techniques as nuclear magnetic resonance, crystallography, electron diffraction or photoaffinity labeling, in conjunction with mutation of putative contact site amino acids. See, for example, de Vos et al., Science 255:306-312, 1992; Smith et al., J. Mol. Biol. 224:899-904, 1992; Wlodaver et al., FEBS Lett. 309:59-64, 1992. The identities of essential amino acids can also be inferred from analysis of homologies with related FGFs and are shown in Figures 1 and 2.

Analyses of the amino acid sequence of zFGF-5 revealed a dibasic site at the C-terminus of the polypeptide (amino acid residue 196-197 (Lys-Arg)). A C-terminally truncated polypeptide comprising an amino acid sequence as shown in SEQ ID NO: 2, from amino acid residue 28 (Glu) to amino acid residue 196 (Lys) was demonstrated to have biological activity. Dibasic amino acids, such as, Arg-X-X-Arg (wherein X is any amino acid residue), Arg-Arg or Lys-Arg; are subject to cleavage by several enzymes, including, but not limited to, thrombin and carboxypeptidases. Therefore, it is within the scope of the claims to make conservative changes at dibasic amino acid residues, in particular the dibasic residues at amino acid residues 196 and 197 (Lys and Arg, respectively) of SEQ ID NO: 2.

Based on analyses of the FGF family a C-terminally truncated molecule that comprises amino acid residue 28 (Glu) to residue 175 (Met) of SEQ ID NO: 2 may be biologically active. An intramolecular disulfide bond

is predicted to occur between amino acid residue 109 (Cys) and residue 129 (Cys) of SEQ ID NO: 2.

Based on homology alignments with FGF-1 and FGF-2 crystal structures (Eriksson et al., Prot. Sci. 2:1274, 1993), secondary structure predictions for beta strand structure of zFGF-5 correlates to amino acid residues 56-59, 64-69, 73-76, 85-92, 96-102, 106-111, 115-119, 128-134, 138-144, 149-155, and 173-177 of SEQ ID NO: 2. Amino acids critical for zFGF-5 binding to receptors can be identified by site-directed mutagenesis of the entire zFGF-5 polypeptide. More specifically, they can be identified using site-directed mutagenesis of amino acids in the zFGF-5 polypeptide which correspond to amino acid residues in acidic FGF (FGF1) and basic FGF (FGF2) identified as critical for binding of these FGFs to their receptors (Blaber et al., Biochem. 35:2086-2094, 1996). These amino acids include Tyr33, Arg53, Asn110, Tyr112, Lys119, Trp123, Leu149 and Met151 in human FGF2, and Tyr30, Arg50, Asn107, Tyr109, Lys116, Trp122, Leu148 and Leu150 in human FGF1, as shown in Fig.1 and Fig.2. The corresponding amino acids in zFGF-5, as shown in Fig.1 and Fig.2, would be Tyr58, Gly77, Asn136, Tyr138, Lys145, Trp149, Met175 and Arg177. One skilled in the art will recognize that other members, in whole or in part, of the FGF family may have structural or biochemical similarities to zFGF-5, and be substituted making such analyses. Such regions would be important for biological functions of the molecule.

Multiple amino acid substitutions can be made and tested using known methods of mutagenesis and screening, such as those disclosed by Reidhaar-Olson and Sauer (Science 241:53-57, 1988) or Bowie and Sauer (Proc. Natl. Acad. Sci. USA 86:2152-2156, 1989). Briefly, these authors disclose methods for simultaneously randomizing two or more positions in a polypeptide, selecting for functional polypeptide, and then sequencing the

mutagenized polypeptides to determine the spectrum of allowable substitutions at each position. Other methods that can be used include phage display (e.g., Lowman et al., Biochem. 30:10832-10837, 1991; Ladner et al., U.S. Patent No. 5,223,409; Huse, WIPO Publication WO 92/06204) and region-directed mutagenesis (Derbyshire et al., Gene 46:145, 1986; Ner et al., DNA 7:127, 1988).

Mutagenesis methods as disclosed above can be combined with high-throughput, automated screening methods to detect activity of cloned, mutagenized polypeptides in host cells. Mutagenized DNA molecules that encode active polypeptides (e.g., cell proliferation) can be recovered from the host cells and rapidly sequenced using modern equipment. These methods allow the rapid determination of the importance of individual amino acid residues in a polypeptide of interest, and can be applied to polypeptides of unknown structure.

Using the methods discussed above, one of ordinary skill in the art can identify and/or prepare a variety of polypeptides that are substantially homologous to residues 28 (Glu) to 196 (Lys) or residues 28 (Glu) to 207 (Ala) of SEQ ID NO: 2, allelic variants thereof, or biologically active fragments thereof, and retain the proliferative properties of the wild-type protein. Such polypeptides may also include additional polypeptide segments as generally disclosed above.

The polypeptides of the present invention, including full-length proteins, fragments thereof and fusion proteins, can be produced in genetically engineered host cells according to conventional techniques. Suitable host cells are those cell types that can be transformed or transfected with exogenous DNA and grown in culture, and include bacteria, fungal cells, and cultured higher eukaryotic cells. Eukaryotic cells, particularly cultured cells of multicellular organisms, are preferred. Techniques for manipulating cloned DNA molecules and

introducing exogenous DNA into a variety of host cells are disclosed by Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989, and Ausubel et al. (eds.), Current Protocols in Molecular Biology, John Wiley and Sons, Inc., NY, 1987, which are incorporated herein by reference.

In general, a DNA sequence encoding a zFGF-5 polypeptide of the present invention is operably linked to other genetic elements required for its expression, generally including a transcription promoter and terminator within an expression vector. The vector will also commonly contain one or more selectable markers and one or more origins of replication, although those skilled in the art will recognize that within certain systems selectable markers may be provided on separate vectors, and replication of the exogenous DNA may be provided by integration into the host cell genome. Selection of promoters, terminators, selectable markers, vectors and other elements is a matter of routine design within the level of ordinary skill in the art. Many such elements are described in the literature and are available through commercial suppliers.

To direct a zFGF-5 polypeptide into the secretory pathway of a host cell, a secretory signal sequence (also known as a leader sequence, prepro sequence or pre sequence) is provided in the expression vector. The secretory signal sequence may be the native sequence, or a chimera comprising a signal sequence derived from another secreted protein (e.g., t-PA and α-pre-pro secretory leader) or synthesized *de novo*. The secretory signal sequence is joined to the zFGF-5 DNA sequence in the correct reading frame. Secretory signal sequences are commonly positioned 5' to the DNA sequence encoding the polypeptide of interest, although certain signal sequences may be positioned elsewhere in the DNA sequence of

interest (see, e.g., Welch et al., U.S. Patent No. 5,037,743; Holland et al., U.S. Patent No. 5,143,830).

A universal acceptor plasmid that can be used to clone a DNA encoding any polypeptide of interest, including polypeptide fusions is disclosed. The acceptor plasmid is useful within a method for preparing a double stranded, circular DNA molecule. The method comprises the steps of (a) providing a double-stranded donor DNA fragment encoding a polypeptide of interest; (b) providing a double-stranded, linear acceptor plasmid having blunt first and second ends and comprising a selectable marker and replication sequence that are functional in *Saccharomyces cerevisiae*, wherein the acceptor plasmid is essentially free of DNA encoding the polypeptide of interest; (c) providing a first double-stranded DNA linker comprising a first segment identical in sequence to a first region of the acceptor plasmid and a second segment identical in sequence to a first region of the donor DNA fragment, wherein each of the first and second segments of the first linker is at least 10 bp in length; (d) providing a second double-stranded DNA linker comprising a first segment identical in sequence to a second region of the acceptor plasmid and a second segment identical in sequence to a second region of the donor DNA fragment, wherein each of the first and second segments of the second linker is at least 10 bp in length; and (e) combining the donor DNA fragment, acceptor plasmid, first DNA linker, and second DNA linker in a *Saccharomyces cerevisiae* host cell whereby the donor DNA fragment is joined to the acceptor plasmid by homologous recombination of the donor DNA, acceptor plasmid, and linkers to form a closed, circular plasmid. The acceptor plasmid further comprises a transcription promoter proximal to the first end, and the donor DNA fragment is operably linked to the transcription promoter within the closed, circular plasmid. The acceptor plasmid further comprises a DNA

segment encoding a leader peptide and/or one or more DNA segments encoding a peptide tag, positioned such that these DNA segments are operably linked to the donor DNA fragment within the closed, circular plasmid. Within a preferred embodiment, the acceptor plasmid further comprises (a) a promoter, a DNA segment encoding a leader peptide, and a DNA segment encoding a first peptide tag, wherein the DNA segment encoding a leader peptide is positioned between the promoter and the DNA segment encoding a first peptide tag proximal to the first end of the acceptor plasmid, wherein the promoter, DNA segment encoding a leader peptide, and DNA segment encoding a first peptide tag are operably linked; and (b) a DNA segment encoding a second peptide tag proximal to the second end of the acceptor plasmid.

A method for preparing a double stranded, circular DNA molecule comprising the steps of (a) providing a plurality of overlapping, double-stranded donor DNA fragments which collectively encode a polypeptide of interest; (b) providing a double-stranded, linear acceptor plasmid having blunt first and second ends and comprising a selectable marker and replication sequence that are functional in *Saccharomyces cerevisiae*, wherein the acceptor plasmid is essentially free of DNA encoding the polypeptide of interest; (c) providing a first double-stranded DNA linker comprising a first segment identical in sequence to a first region of the acceptor plasmid and a second segment identical in sequence to a first region of one of the donor DNA fragments, wherein each of the first and second segments of the first linker is at least 10 bp in length; (d)

providing a second double-stranded DNA linker comprising a first segment identical in sequence to a second region of the acceptor plasmid and a second segment identical in sequence to a region of another of the donor DNA fragments, wherein each of the first and second

segments of the second linker is at least 10 bp in length; and (e) combining the donor DNA fragments, acceptor plasmid, first DNA linker, and second DNA linker in a *Saccharomyces cerevisiae* host cell whereby the donor DNA fragments are joined to the acceptor plasmid by homologous recombination to form a closed, circular plasmid comprising a region encoding the polypeptide of interest is disclosed. The acceptor plasmid further comprises one or more of a transcription promoter, a DNA segment encoding a leader peptide, and one or more DNA segments encoding a peptide tag as disclosed above.

Fungal cells, including yeast cells, and particularly cells of the genera *Saccharomyces* or *Pichia*, are particularly preferred cells for hosts for producing zFGF-5 fragments or polypeptide fusions.

Other methods for transforming yeast cells with exogenous DNA and producing recombinant polypeptides therefrom are disclosed by, for example, Kawasaki, U.S. Patent No. 4,599,311; Kawasaki et al., U.S. Patent No. 4,931,373; Brake, U.S. Patent No. 4,870,008; Welch et al., U.S. Patent No. 5,037,743; and Murray et al., U.S. Patent No. 4,845,075, which are incorporated herein by reference. Transformed cells are selected by phenotype determined by the selectable marker, commonly drug resistance or the ability to grow in the absence of a particular nutrient (e.g., leucine). An alternative preferred vector system for use in yeast is the POT1 vector system disclosed by Kawasaki et al. (U.S. Patent No. 4,931,373), which allows transformed cells to be selected by growth in glucose-containing media. Suitable promoters and terminators for use in yeast include those from glycolytic enzyme genes (see, e.g., Kawasaki, U.S. Patent No. 4,599,311; Kingsman et al., U.S. Patent No. 4,615,974; and Bitter, U.S. Patent No. 4,977,092, which are incorporated herein by reference) and alcohol dehydrogenase genes. See also U.S. Patents Nos. 4,990,446; 5,063,154; 5,139,936 and 4,661,454, which

are incorporated herein by reference. Transformation systems for other yeasts, including *Hansenula polymorpha, Schizosaccharomyces pombe, Kluyveromyces lactis, Kluyveromyces fragilis, Ustilago maydis, Pichia pastoris, Pichia guillermondii,* and *Candida maltosa* are known in the art. A particularly preferred system utilizes *Pichia methanolica* (see, PCT application WO 9717450). For alternative transformation systems, see, for example, Gleeson et al., J. Gen. Microbiol. 132:3459-3465, 1986 and Cregg, U.S. Patent No. 4,882,279. *Aspergillus* cells may be utilized according to the methods of McKnight et al., U.S. Patent No. 4,935,349, which is incorporated herein by reference. Methods for transforming *Acremonium chrysogenum* are disclosed by Sumino et al., U.S. Patent No. 5,162,228, which is incorporated herein by reference. Methods for transforming *Neurospora* are disclosed by Lambowitz, U.S. Patent No. 4,486,533, which is incorporated herein by reference.

Cultured mammalian cells are also preferred hosts within the present invention. Methods for introducing exogenous DNA into mammalian host cells include calcium phosphate-mediated transfection (Wigler et al., Cell 14:725, 1978; Corsaro and Pearson, Somatic Cell Genetics 7:603, 1981: Graham and Van der Eb, Virology 52:456, 1973), electroporation (Neumann et al., EMBO J. 1:841-845, 1982), DEAE-dextran mediated transfection (Ausubel et al., eds., Current Protocols in Molecular Biology, John Wiley and Sons, Inc., NY, 1987), and liposome-mediated transfection (Hawley-Nelson et al., Focus 15:73, 1993; Ciccarone et al., Focus 15:80, 1993), which are incorporated herein by reference. The production of recombinant polypeptides in cultured mammalian cells is disclosed, for example, by Levinson et al., U.S. Patent No. 4,713,339; Hagen et al., U.S. Patent No. 4,784,950; Palmiter et al., U.S. Patent No. 4,579,821; and Ringold, U.S. Patent No. 4,656,134, which are

incorporated herein by reference. Preferred cultured mammalian cells include the COS-1 (ATCC No. CRL 1650), COS-7 (ATCC No. CRL 1651), BHK 570 (ATCC No. CRL 10314), 293 (ATCC No. CRL 1573; Graham et al., J. Gen. Virol. 36:59-72, 1977) and Chinese hamster ovary (e.g. CHO-K1; ATCC No. CCL 61) cell lines. Additional suitable cell lines are known in the art and available from public depositories such as the American Type Culture Collection, Rockville, Maryland. In general, strong transcription promoters are preferred, such as promoters from SV-40 or cytomegalovirus. See, e.g., U.S. Patent No. 4,956,288. Other suitable promoters include those from metallothionein genes (U.S. Patent Nos. 4,579,821 and 4,601,978, which are incorporated herein by reference) and the adenovirus major late promoter.

Drug selection is generally used to select for cultured mammalian cells into which foreign DNA has been inserted. Such cells are commonly referred to as "transfectants". Cells that have been cultured in the presence of the selective agent and are able to pass the gene of interest to their progeny are referred to as "stable transfectants." A preferred selectable marker is a gene encoding resistance to the antibiotic neomycin. Selection is carried out in the presence of a neomycin-type drug, such as G-418 or the like. Selection systems may also be used to increase the expression level of the gene of interest, a process referred to as "amplification." Amplification is carried out by culturing transfectants in the presence of a low level of the selective agent and then increasing the amount of selective agent to select for cells that produce high levels of the products of the introduced genes. A preferred amplifiable selectable marker is dihydrofolate reductase, which confers resistance to methotrexate. Other drug resistance genes (e.g., hygromycin resistance,

multi-drug resistance, puromycin acetyltransferase) can also be used.

Other higher eukaryotic cells can also be used as hosts, including insect cells, plant cells and avian cells. Transformation of insect cells and production of foreign polypeptides therein is disclosed by Guarino et al., U.S. Patent No. 5,162,222; Bang et al., U.S. Patent No. 4,775,624; and WIPO publication WO 94/06463, which are incorporated herein by reference. The use of *Agrobacterium rhizogenes* as a vector for expressing genes in plant cells has been reviewed by Sinkar et al., J. Biosci. (Bangalore) 11:47-58, 1987.

Transformed or transfected host cells are cultured according to conventional procedures in a culture medium containing nutrients and other components required for the growth of the chosen host cells. A variety of suitable media, including defined media and complex media, are known in the art and generally include a carbon source, a nitrogen source, essential amino acids, vitamins and minerals. Media may also contain such components as growth factors or serum, as required. The growth medium will generally select for cells containing the exogenously added DNA by, for example, drug selection or deficiency in an essential nutrient which is complemented by the selectable marker carried on the expression vector or co-transfected into the host cell.

Expressed recombinant zFGF-5 polypeptides (or chimeric zFGF-5 polypeptides) can be purified using fractionation and/or conventional purification methods and media. Ammonium sulfate precipitation and acid or chaotrope extraction may be used for fractionation of samples. Exemplary purification steps may include hydroxyapatite, size exclusion, FPLC and reverse-phase high performance liquid chromatography. Suitable anion exchange media include derivatized dextrans, agarose, cellulose, polyacrylamide, specialty silicas, and the

like. PEI, DEAE, QAE and Q derivatives are preferred, with DEAE Fast-Flow Sepharose (Pharmacia, Piscataway, NJ) being particularly preferred. Exemplary chromatographic media include those media derivatized with phenyl, butyl, or octyl groups, such as Phenyl-Sepharose FF (Pharmacia), Toyopearl butyl 650 (Toso Haas, Montgomeryville, PA), Octyl-Sepharose (Pharmacia) and the like; or polyacrylic resins, such as Amberchrom CG 71 (Toso Haas) and the like. Suitable solid supports include glass beads, silica-based resins, cellulosic resins, agarose beads, cross-linked agarose beads, polystyrene beads, cross-linked polyacrylamide resins and the like that are insoluble under the conditions in which they are to be used. These supports may be modified with reactive groups that allow attachment of proteins by amino groups, carboxyl groups, sulfhydryl groups, hydroxyl groups and/or carbohydrate moieties. Examples of coupling chemistries include cyanogen bromide activation, N-hydroxysuccinimide activation, epoxide activation, sulfhydryl activation, hydrazide activation, and carboxyl and amino derivatives for carbodiimide coupling chemistries. These and other solid media are well known and widely used in the art, and are available from commercial suppliers. Methods for binding receptor polypeptides to support media are well known in the art. Selection of a particular method is a matter of routine design and is determined in part by the properties of the chosen support. See, for example, Affinity Chromatography: Principles & Methods, Pharmacia LKB Biotechnology, Uppsala, Sweden, 1988.

The polypeptides of the present invention can also be isolated by exploitation of their heparin binding properties. For a review, see, Burgess et al., Ann. Rev. of Biochem. 58:575-606, 1989. Members of the FGF family can be purified to apparent homogeneity by heparin-Sepharose affinity chromatography (Gospodarowicz et al., Proc. Natl. Acad. Sci. 81:6963-6967, 1984) and eluted

using linear step gradients of NaCl (Ron et al., J. Biol. Chem. 268(4):2984-2988, 1993; Chromatography: Principles & Methods, pp. 77-80, Pharmacia LKB Biotechnology, Uppsala, Sweden, 1993; in "Immobilized Affinity Ligand Techniques", Hermanson et al., eds., pp. 165-167, Academic Press, San Diego, 1992; Kjellen et al., Ann. Rev. Biochem.Ann. Rev. Biochem. 60:443-474, 1991; and Ke et al., Protein Expr. Purif. 3(6):497-507, 1992.)

Other purification methods include using immobilized metal ion adsorption (IMAC) chromatography to purify histidine-rich proteins. Briefly, a gel is first charged with divalent metal ions to form a chelate (E. Sulkowski, Trends in Biochem. 3:1-7, 1985). Histidine-rich proteins will be adsorbed to this matrix with differing affinities, depending upon the metal ion used, and will be eluted by competitive elution, lowering the pH, or use of strong chelating agents. Other methods of purification include purification of glycosylated proteins by lectin affinity chromatography and ion exchange chromatography (Methods in Enzymol., Vol. 182, "Guide to Protein Purification", M. Deutscher, (ed.), Acad. Press, San Diego, 1990, pp.529-39). Alternatively, a fusion of the polypeptide of interest and an affinity tag (e.g., polyhistidine, maltose-binding protein, an immunoglobulin domain) may be constructed to facilitate purification.

Protein refolding (and optionally reoxidation) procedures may be advantageously used. It is preferred to purify the protein to >80% purity, more preferably to >90% purity, even more preferably >95%, and particularly preferred is a pharmaceutically pure state, that is greater than 99.9% pure with respect to contaminating macromolecules, particularly other proteins and nucleic acids, and free of infectious and pyrogenic agents. Preferably, a purified protein is substantially free of other proteins, particularly other proteins of animal origin.

zFGF-5 polypeptides or fragments thereof may also be prepared through chemical synthesis. zFGF-5 polypeptides may be monomers or multimers; glycosylated or non-glycosylated; pegylated or non-pegylated; and may or may not include an initial methionine amino acid residue.

The activity of molecules of the present invention can be measured using a variety of assays that, for example, measure neogenesis or hyperplasia (i.e., proliferation) of cardiac cells based on the tissue specificity in adult heart. Additional activities likely associated with the polypeptides of the present invention include proliferation of endothelial cells, cardiomyocytes, fibroblasts, skeletal myocytes directly or indirectly through other growth factors; action as a chemotaxic factor for endothelial cells, fibroblasts and/or phagocytic cells; osteogenic factor; and factor for expanding mesenchymal stem cell and precursor populations.

Proliferation can be measured using cultured cardiac cells or *in vivo* by administering molecules of the claimed invention to the appropriate animal model. Generally, proliferative effects are seen as an increase in cell number and therefore, may include inhibition of apoptosis, as well as mitogenesis. Cultured cells include cardiac fibroblasts, cardiac myocytes, skeletal myocytes, human umbilical vein endothelial cells from primary cultures. Established cell lines include: NIH 3T3 fibroblast (ATCC No. CRL-1658), CHH-1 chum heart cells (ATCC No. CRL-1680), H9c2 rat heart myoblasts (ATCC No. CRL-1446), Shionogi mammary carcinoma cells (Tanaka et al., Proc. Natl. Acad. Sci. 89:8928-8932, 1992) and LNCap.FGC adenocarcinoma cells (ATCC No. CRL-1740.) Assays measuring cell proliferation are well known in the art. For example, assays measuring proliferation include such assays as chemosensitivity to neutral red dye (Cavanaugh et al., Investigational New Drugs 8:347-354, 1990, incorporated herein by reference), incorporation of

radiolabelled nucleotides (Cook et al., Analytical Biochem. 179:1-7, 1989, incorporated herein by reference), incorporation of 5-bromo-2'-deoxyuridine (BrdU) in the DNA of proliferating cells (Porstmann et al., J. Immunol. Methods 82:169-179, 1985, incorporated herein by reference), and use of tetrazolium salts (Mosmann, J. Immunol. Methods 65:55-63, 1983; Alley et al., Cancer Res. 48:589-601, 1988; Marshall et al., Growth Reg. 5:69-84, 1995; and Scudiero et al., Cancer Res. 48:4827-4833, 1988; all incorporated herein by reference).

Differentiation is a progressive and dynamic process, beginning with pluripotent stem cells and ending with terminally differentiated cells. Pluripotent stem cells that can regenerate without commitment to a lineage express a set of differentiation markers that are lost when commitment to a cell lineage is made. Progenitor cells express a set of differentiation markers that may or may not continue to be expressed as the cells progress down the cell lineage pathway toward maturation. Differentiation markers that are expressed exclusively by mature cells are usually functional properties such as cell products, enzymes to produce cell products and receptors. The stage of a cell population's differentiation is monitored by identification of markers present in the cell population. Myocytes, osteoblasts, adipocytes, chrondrocytes, fibroblasts and reticular cells are believed to originate from a common mesenchymal stem cell (Owen et al., Ciba Fdn. Symp. 136:42-46, 1988). Markers for mesenchymal stem cells have not been well identified (Owen et al., J. of Cell Sci. 87:731-738, 1987), so identification is usually made at the progenitor and mature cell stages. The existence of early stage cardiac myocyte progenitor cells (often referred to as cardiac myocyte stem cells) has been speculated, but not demonstrated, in adult cardiac tissue. The novel polypeptides of the present invention are useful for

studies to isolate mesenchymal stem cells and cardiac myocyte progenitor cells, both *in vivo* and *ex vivo*.

There is evidence to suggest that factors that stimulate specific cell types down a pathway towards terminal differentiation or dedifferentiation, affects the entire cell population originating from a common precursor or stem cell. Thus, the present invention includes stimulating inhibition or proliferation of myocytes, smooth muscle cells, osteoblasts, adipocytes, chrondrocytes and endothelial cells. Molecules of the present invention may, while stimulating proliferation or differentiation of cardiac myocytes, inhibit proliferation or differentiation of adipocytes, by virtue of the affect on their common precursor/stem cells. Thus molecules of the present invention, have use in inhibiting chondrosarcomas, atherosclerosis, restenosis and obesity.

Assays measuring differentiation include, for example, measuring cell-surface markers associated with stage-specific expression of a tissue, enzymatic activity, functional activity or morphological changes (Watt, FASEB, 5:281-284, 1991; Francis, Differentiation 57:63-75, 1994; Raes, Adv. Anim. Cell Biol. Technol. Bioprocesses, 161-171, 1989; all incorporated herein by reference).

In vivo assays for evaluating cardiac neogenesis or hyperplasia include treating neonatal and mature rats with the molecules of the present invention. The animals cardiac function is measured as heart rate, blood pressure, and cardiac output to determine left ventricular function. Post-mortem methods for assessing cardiac improvement include: increased cardiac weight, nuclei/cytoplasmic volume, staining of cardiac histology sections to determine proliferating cell nuclear antigen (PCNA) vs. cytoplasmic actin levels (Quaini et al., Circulation Res. 75:1050-1063, 1994 and Reiss et al., Proc. Natl. Acad. Sci. 93:8630-8635, 1996.)

In vivo assays for measuring changes in bone formation rates include performing bone histology (see, Recker, R., eds. Bone Histomorphometry: Techniques and Interpretation. Boca Raton: CRC Press, Inc., 1983) and quantitative computed tomography (QCT; Ferretti,J. Bone 17:353S-364S, 1995; Orphanoludakis et al., Investig. Radiol. 14:122-130,, 1979 and Durand et al., Medical Physics 19:569-573, 1992). An *ex vivo* assay for measuring changes in bone formation would be, for example, a calavarial assay (Gowen et al., J. Immunol. 136:2478-2482, 1986).

With regard to modulating energy balance, particularly as it relates to adipocyte metabolism, proliferation and differentiation, zFGF-5 polypeptides modulate effects on metabolic reactions. Such metabolic reactions include adipogenesis, gluconeogenesis, glycogenolysis, lipogenesis, glucose uptake, protein synthesis, thermogenesis, oxygen utilization and the like. Among other methods known in the art or described herein, mammalian energy balance may be evaluated by monitoring one or more of the aforementioned metabolic functions. These metabolic functions are monitored by techniques (assays or animal models) known to one of ordinary skill in the art, as is more fully set forth below. For example, the glucoregulatory effects of insulin are predominantly exerted in the liver, skeletal muscle and adipose tissue. In skeletal muscle and adipose tissue, insulin acts to stimulate the uptake, storage and utilization of glucose.

Art-recognized methods exist for monitoring all of the metabolic functions recited above. Thus, one of ordinary skill in the art is able to evaluate zFGF-5 polypeptides, fragments, fusion proteins, antibodies, agonists and antagonists for metabolic modulating functions. Exemplary modulating techniques are set forth below.

Insulin-stimulated lipogenesis, for example, may be monitored by measuring the incorporation of ^{14}C-acetate into triglyceride (Mackall et al. J. Biol. Chem. 251:6462-6464, 1976) or triglyceride accumulation (Kletzien et al., Mol. Pharmacol. 41:393-398, 1992).

zFGF-5-stimulated uptake may be evaluated, for example, in an assay for insulin-stimulated glucose transport. Primary adipocytes or NIH 3T3 L1 cells (ATCC No. CCL-92.1) are placed in DMEM containing 1 g/l glucose, 0.5 or 1.0% BSA, 20 mM Hepes, and 2 mM glutamine. After two to five hours of culture, the medium is replaced with fresh, glucose-free DMEM containing 0.5 or 1.0% BSA, 20 mM Hepes, 1 mM pyruvate, and 2 mM glutamine. Appropriate concentrations of zFGF-5, insulin or IGF-1, or a dilution series of the test substance, are added, and the cells are incubated for 20-30 minutes. ^{3}H or ^{14}C-labeled deoxyglucose is added to ≈50 lM final concentration, and the cells are incubated for approximately 10-30 minutes. The cells are then quickly rinsed with cold buffer (e.g. PBS), then lysed with a suitable lysing agent (e.g. 1% SDS or 1 N NaOH). The cell lysate is then evaluated by counting in a scintillation counter. Cell-associated radioactivity is taken as a measure of glucose transport after subtracting non-specific binding as determined by incubating cells in the presence of cytocholasin b, an inhibitor of glucose transport. Other methods include those described by, for example, Manchester et al., Am. J. Physiol. 266 (Endocrinol. Metab. 29):E326-E333, 1994 (insulin-stimulated glucose transport).

Protein synthesis may be evaluated, for example, by comparing precipitation of ^{35}S-methionine-labeled proteins following incubation of the test cells with ^{35}S-methionine and ^{35}S-methionine and a putative modulator of protein synthesis.

Thermogenesis may be evaluated as described by B. Stanley in *The Biology of Neuropeptide Y and Related*

Peptides, W. Colmers and C. Wahlestedt (eds.), Humana Press, Ottawa, 1993, pp. 457-509; C. Billington et al., Am. J. Physiol. 260:R321, 1991; N. Zarjevski et al., Endocrinology 133:1753, 1993; C. Billington et al., Am. J. Physiol. 266:R1765, 1994; Heller et al., Am. J. Physiol. 252(4 Pt 2): R661-7, 1987; and Heller et al., Am. J. Physiol. 245(3): R321-8, 1983. Also, metabolic rate, which may be measured by a variety of techniques, is an indirect measurement of thermogenesis.

Oxygen utilization may be evaluated as described by Heller et al., Pflugers Arch 369(1): 55-9, 1977. This method also involved an analysis of hypothalmic temperature and metabolic heat production. Oxygen utilization and thermoregulation have also been evaluated in humans as described by Haskell et al., J. Appl. Physiol. 51(4): 948-54, 1981.

zFGF-5 polypeptides can also be used to prepare antibodies that specifically bind to zFGF-5 epitopes, peptides or polypeptides. Methods for preparing polyclonal and monoclonal antibodies are well known in the art (see, for example, Sambrook et al., Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, NY, 1989; and Hurrell, J. G. R., Ed., Monoclonal Hybridoma Antibodies: Techniques and Applications, CRC Press, Inc., Boca Raton, FL, 1982, which are incorporated herein by reference). As would be evident to one of ordinary skill in the art, polyclonal antibodies can be generated from a variety of warm-blooded animals, such as horses, cows, goats, sheep, dogs, chickens, rabbits, mice, and rats.

The immunogenicity of a zFGF-5 polypeptide may be increased through the use of an adjuvant, such as alum (aluminum hydroxide) or Freund's complete or incomplete adjuvant. Polypeptides useful for immunization also include fusion polypeptides, such as fusions of zFGF-5 or a portion thereof with an immunoglobulin polypeptide or with maltose binding protein. The polypeptide immunogen

may be a full-length molecule or a portion thereof. If the polypeptide portion is "hapten-like", such portion may be advantageously joined or linked to a macromolecular carrier (such as keyhole limpet hemocyanin (KLH), bovine serum albumin (BSA) or tetanus toxoid) for immunization.

As used herein, the term "antibodies" includes polyclonal antibodies, affinity-purified polyclonal antibodies, monoclonal antibodies, and antigen-binding fragments, such as $F(ab')_2$ and Fab proteolytic fragments. Genetically engineered intact antibodies or fragments, such as chimeric antibodies, Fv fragments, single chain antibodies and the like, as well as synthetic antigen-binding peptides and polypeptides, are also included. Non-human antibodies may be humanized by grafting only non-human CDRs onto human framework and constant regions, or by incorporating the entire non-human variable domains (optionally "cloaking" them with a human-like surface by replacement of exposed residues, wherein the result is a "veneered" antibody). In some instances, humanized antibodies may retain non-human residues within the human variable region framework domains to enhance proper binding characteristics. Through humanizing antibodies, biological half-life may be increased, and the potential for adverse immune reactions upon administration to humans is reduced. Alternative techniques for generating or selecting antibodies useful herein include *in vitro* exposure of lymphocytes to zFGF-5 protein or peptide, and selection of antibody display libraries in phage or similar vectors (for instance, through use of immobilized or labeled zFGF-5 protein or peptide).

Antibodies are defined to be specifically binding if they bind to a zFGF-5 polypeptide with a binding affinity (K_a) of 10^6 M^{-1} or greater, preferably 10^7 M^{-1} or greater, more preferably 10^8 M^{-1} or greater, and most preferably 10^9 M^{-1} or greater. The binding affinity of an

antibody can be readily determined by one of ordinary skill in the art (for example, by Scatchard analysis).

A variety of assays known to those skilled in the art can be utilized to detect antibodies which specifically bind to zFGF-5 proteins or peptides. Exemplary assays are described in detail in Antibodies: A Laboratory Manual, Harlow and Lane (Eds.), Cold Spring Harbor Laboratory Press, 1988. Representative examples of such assays include: concurrent immunoelectrophoresis, radioimmunoassay, radioimmuno-precipitation, enzyme-linked immunosorbent assay (ELISA), dot blot or Western blot assay, inhibition or competition assay, and sandwich assay. In addition, antibodies can be screened for binding to wild-type versus mutant zFGF-5 protein or peptide.

Antibodies to zFGF-5 may be used for tagging cells that express zFGF-5; to target another protein, small molecule or chemical to heart tissue; for isolating zFGF-5 by affinity purification; for diagnostic assays for determining circulating levels of zFGF-5 polypeptides; for detecting or quantitating soluble zFGF-5 as marker of underlying pathology or disease; in analytical methods employing FACS; for screening expression libraries; for generating anti-idiotypic antibodies; and as neutralizing antibodies or as antagonists to block zFGF-5 mediated proliferation *in vitro* and *in vivo*. Suitable direct tags or labels include radionuclides, enzymes, substrates, cofactors, inhibitors, fluorescent markers, chemiluminescent markers, magnetic particles and the like; indirect tags or labels may feature use of biotin-avidin or other complement/anti-complement pairs as intermediates. Antibodies herein may also be directly or indirectly conjugated to drugs, toxins, radionuclides and the like, and these conjugates used for *in vivo* diagnostic or therapeutic applications.

Molecules of the present invention can be used to identify and isolate receptors involved in cardiac myocardial proliferation. For example, proteins and peptides of the present invention can be immobilized on a column and membrane preparations run over the column (Immobilized Affinity Ligand Techniques, Hermanson et al., eds., Academic Press, San Diego, CA, 1992, pp.195-202). Proteins and peptides can also be radiolabeled (Methods in Enzymol., vol. 182, "Guide to Protein Purification", M. Deutscher, ed., Acad. Press, San Diego, 1990, 721-737) or photoaffinity labeled (Brunner et al., Ann. Rev. Biochem. 62:483-514, 1993 and Fedan et al., Biochem. Pharmacol. 33:1167-1180, 1984) and specific cell-surface proteins can be identified.

Antagonists will be useful for inhibiting the proliferative activities of zFGF-5 molecules, in cell types such as cardiac cells, including myocytes, fibroblasts and endothelial cells; osteoblasts and chrondrocytes. Genes encoding zFGF-5 polypeptide binding domains can be obtained by screening random peptide libraries displayed on phage (phage display) or on bacteria, such as *E. coli*. Nucleotide sequences encoding the polypeptides can be obtained in a number of ways, such as through random mutagenesis and random polynucleotide synthesis. These random peptide display libraries can be used to screen for peptides which interact with a known target which can be a protein or polypeptide, such as a ligand or receptor, a biological or synthetic macromolecule, or organic or inorganic substances. Techniques for creating and screening such random peptide display libraries are known in the art (Ladner et al., US Patent NO:5,223,409; Ladner et al., US Patent NO:4,946,778; Ladner et al., US Patent NO:5,403,484 and Ladner et al., US Patent NO:5,571,698) and random peptide display libraries and kits for screening such libraries are available commercially, for instance from Clontech

(Palo Alto, CA), Invitrogen Inc. (San Diego, CA), New England Biolabs, Inc. (Beverly, MA) and Pharmacia LKB Biotechnology Inc. (Piscataway, NJ). Random peptide display libraries can be screened using the zFGF-5 sequences disclosed herein to identify proteins which bind to zFGF-5. These "binding proteins" which interact with zFGF-5 polypeptides may be used for tagging cells; for isolating homolog polypeptides by affinity purification; they can be directly or indirectly conjugated to drugs, toxins, radionuclides and the like. These binding proteins can also be used in analytical methods such as for screening expression libraries and neutralizing activity. The binding proteins can also be used for diagnostic assays for determining circulating levels of polypeptides; for detecting or quantitating soluble polypeptides as marker of underlying pathology or disease. These binding proteins can also act as zFGF-5 "antagonists" to block zFGF-5 binding and signal transduction *in vitro* and *in vivo*. These anti- zFGF-5 binding proteins would be useful for inhibiting expression of genes which result in proliferation or differentiation. Such anti-zFGF-5 binding proteins can be used for treatment, for example, in rhabdomyosarcoma, cardiac myxoma, bone cancers of osteoblast origin, and dwarfism, arthritis, ligament and cartilage repair, alone or combination with other therapies.

The molecules of the present invention will be useful for proliferation of cardiac tissue cells, such as cardiac myocytes or myoblasts; skeletal myocytes or myoblasts and smooth muscle cells; chrondrocytes; endothelial cells; adipocytes and osteoblasts *in vitro*. For example, molecules of the present invention are useful as components of defined cell culture media, and may be used alone or in combination with other cytokines and hormones to replace serum that is commonly used in cell culture. Molecules of the present invention are

particularly useful in specifically promoting the growth and/or development of myocytes in culture, and may also prove useful in the study of cardiac myocyte hyperplasia and regeneration.

The polypeptides, nucleic acid and/or antibodies of the present invention may be used in treatment of disorders associated with myocardial infarction, congestive heart failure, hypertrophic cardiomyopathy and dilated cardiomyopathy. Molecules of the present invention may also be useful for limiting infarct size following a heart attack, promoting angiogenesis and wound healing following angioplasty or endarterectomy, to develop coronary collateral circulation, for revascularization in the eye, for complications related to poor circulation such as diabetic foot ulcers, for stroke; following coronary reperfusion using pharmacologic methods and other indications where angiogenesis is of benefit. Molecules of the present invention may be useful for improving cardiac function, either by inducing cardiac myocyte neogenesis and/or hyperplasia, by inducing coronary collateral formation, or by inducing remodelling of necrotic myocardial area. Other therapeutic uses for the present invention include induction of skeletal muscle neogenesis and/or hyperplasia, kidney regeneration and/or for treatment of systemic and pulmonary hypertension.

zFGF-5 induced coronary collateral development is measured in rabbits, dogs or pigs using models of chronic coronary occlusion (Landau et al., Amer. Heart J. 29:924-931, 1995; Sellke et al., Surgery 120(2):182-188, 1996 and Lazarous et al., 1996, ibid.) zFGF-5 benefits for treating stroke is tested *in vivo* in rats utilizing bilateral carotid artery occlusion and measuring histological changes, as well as maze performance (Gage et al., Neurobiol. Aging 9:645-655, 1988). zFGF-5 efficacy in hypertension is tested *in vivo* utilizing spontaneously hypertensive rats (SHR) for systemic hypertension (Marche

et al., Clin. Exp. Pharmacol. Physiol. Suppl. 1:S114-116, 1995).

Molecules of the present invention can be used to target the delivery of agents or drugs to the heart. For example, the molecules of the present invention will be useful limiting expression to the heart, by virtue of the tissue specific expression directed by the zFGF-5 promoter. For example, heart-specific expression can be achieved using a zFGF-5-adenoviral discistronic construct (Rothmann et al., Gene Therapy 3:919-926, 1996). In addition, the zFGF-5 polypeptides can be used to restrict other agents or drugs to heart tissue by linking zFGF-5 polypeptides to another protein (Franz et al., Circ. Res. 73:629-638, 1993) by linking a first molecule that is comprised of a zFGF-5 homolog polypeptide with a second agent or drug to form a chimera. Proteins, for instance antibodies, can be used to form chimeras with zFGF-5 molecules of the present invention (Narula et al., J. Nucl. Cardiol. 2:26-34, 1995). Examples of agents or drugs include, but are not limited to, bioactive-polypeptides, genes, toxins, radionuclides, small molecule pharmaceuticals and the like. Linking may be direct or indirect (e.g., liposomes), and may occur by recombinant means, chemical linkage, strong non-covalent interaction and the like.

In one embodiment of the present invention, a composition comprising zFGF-5 protein is used as a therapeutic agent to enhance osteoblast-mediated bone formation. The compositions and methods using the compositions of the invention may be applied to promote the repair of bone defects and deficiencies, such as those occurring in closed, open and non-union fractures; to promote bone healing in plastic surgery; to stimulate bone ingrowth into non-cemented prosthetic joints and dental implants; in the treatment of periodontal disease and defects; to increase bone formation during distraction

osteogenesis; and in treatment of other skeletal disorders that may be treated by stimulation of osteoblastic activity, such as osteoporosis and arthritis. *De novo* bone formation provided by the methods of the present invention will have use in repair of congenital, trauma-induced, oncologic resection of bone or healing bone following radiation-induced osteonecrosis (Hart et al, Cancer 37:2580-2585, 1976). The methods of the present invention may also find use in plastic surgery.

For pharmaceutical use, the proteins of the present invention are formulated for parenteral, particularly intravenous or subcutaneous, administration according to conventional methods. Intravenous administration will be by bolus injection or infusion over a typical period of one to several hours. In general, pharmaceutical formulations will include a zFGF-5 protein in combination with a pharmaceutically acceptable vehicle, such as saline, buffered saline, 5% dextrose in water or the like. Formulations may further include one or more excipients, preservatives, solubilizers, buffering agents, albumin to prevent protein loss on vial surfaces, etc. Methods of formulation are well known in the art and are disclosed, for example, in Remington's Pharmaceutical Sciences, Gennaro, ed., Mack Publishing Co., Easton PA, 1990, which is incorporated herein by reference. Therapeutic doses will generally be in the range of 0.1 to 100 μg/kg of patient weight per day, preferably 0.5-20 μg/kg per day, with the exact dose determined by the clinician according to accepted standards, taking into account the nature and severity of the condition to be treated, patient traits, etc. Determination of dose is within the level of ordinary skill in the art. The proteins may be administered for acute treatment, over one week or less, often over a period of one to three days or may be used in chronic treatment, over several months or years. In general, a therapeutically effective amount of

zFGF-5 is an amount sufficient to produce a clinically significant change in myocyte proliferation, heart function, bone formation or increases in specific cell types associated with mesenchymal stem cells and progenitors for myocytes, osteoblasts and chrondocytes. In particular, a clinical significant increase in the number of myocytes or myocyte progenitor cells can be determined by measuring the left ventricular ejection fraction, prior to, and after administration of zFGF-5 molecules, and determining at least a 5% increase, preferably 10% or more, in the total ejection fraction. Tests to determine ejection fraction, as measured by blood ejected per beat, are well known to those ordinarily skilled in the art.

The invention is further illustrated by the following non-limiting examples.

EXAMPLES

Example 1

Extension of EST Sequence

Scanning of a translated DNA database using a query for growth factors resulted in identification of an expressed sequence tag (EST) sequence found to be a novel member of the FGF family, and designated zFGF-5.

Oligonucleotide primers ZC11,676 (SEQ ID NO: 3) and ZC11,677 (SEQ ID NO: 4) were designed from the sequence of an expressed sequence tag (EST). The primers were used for priming internally within the EST, and when PCR was performed using MARATHON READY cDNA (Clontech, Palo Alto, CA) from adult heart tissue as template in polymerase chain reaction (PCR).

The conditions used for PCR were 1 cycle at 94°C for 90 seconds, 35 cycles at 94°C for 15 seconds; 68°C for 1 minute; followed by 1 cycle for 10 minutes at 72°C and 4° C incubation period. The PCR reaction recreated 160 bp of

the EST sequence, and confirmed that EST sequence was correct.

Other libraries that could be amplified with the oligonucleotide primers included skeletal muscle, lung, stomach, small intestine and thyroid.

Example 2
Tissue Distribution

Northerns were performed using Human Multiple Tissue Blots from Clontech (Palo Alto, CA). The 160 bp DNA fragment described in Example 1 was electrophoresed on a 1% agarose gel, the fragment was electroeluted, and then radioactively labeled using a randon priming MEGAPRIME DNA labeling system (Amersham, Arlington Heights, IL) according to the manufacturer's specifications. The probe was purified using a NUCTRAP push column (Stratagene Cloning Systems, La Jolla, CA). EXPRESSHYB (Clontech, Palo Alto, CA) solution was used for prehybridization and as a hydrizing solution for the Northern blots. Hybridization took place overnight at 68°C, and the blots were then washed in 2X SSC and 0.05% SDS at RT, followed by a wash in 0.1X SSC and 0.1% SDS at 50°C. A single band was observed at approximately 2.0 kb. Signal intensity was highest for adult heart with relatively less intense signals in skeletal muscle and stomach.

Example 3
Assay for *In Vitro* Activity of zFGF-5

A.

The mitogenic activity of zFGF-5 is assayed using cell lines and cells from a primary culture. Conditioned medium from cells expressing the recombinant protein and/or purified protein is added to cultures of the following cell lines: NIH 3T3 fibroblast (ATCC No. CRL-1658), CHH-1 chum heart cells (ATCC No. CRL-1680), H9c2 rat heart myoblasts (ATCC No. CRL-1446), Shionogi

mammary carcinoma cells (Tanaka et al., 1992, ibid.) and LNCaP.FGC adenocarcinoma cells. Freshly isolated cells useful for testing the proliferative activity of zFGF-5 include: cardiac fibroblasts, cardiac myocytes, skeletal myocytes and human umbilical vein endothelial cells.

Mitogenic activity is assayed by measurement of ^{3}H-thymidine incorporation based on the method of Raines and Ross (Meth. Enzymology 109:749-773, 1985). Briefly, quiescent cells are plated cells at a density of 3 x 10^4 cells/ml in an appropriate medium. A typical growth medium is Dulbecco's Growth Medium (GIBCO-BRL, Gaithersburg, MD) containing 10% fetal calf serum (FCS). The cells are cultured in 96-well plates and allowed to grow for 3-4 days. The growth medium is removed, and 180 µl of DFC (Table 5) containing 0.1% FCS is added per well. Half the wells have zFGF-5 protein added to them and the other half are a negative control, without zFGF-5. The cells are incubated for up to 3 days at 37°C in 5% CO_2, and the medium is removed. One hundred microliters of DFC containing 0.1% FCS and 2 µCi/ml ^{3}H-thymidine is added to each well, and the plates are incubated an additional 1-24 hours at 37°C . The medium is aspirated off, and 150 µl of trypsin is added to each well. The plates are incubated at 37°C until the cells detached (at least 10 minutes). The detached cells are harvested onto filters using an LKB Wallac 1295-001 Cell Harvester (LKB Wallac, Pharmacia, Gaithersburg, MD). The filters are dried by heating in a microwave oven for 10 minutes and counted in an LKB Betaplate 1250 scintillation counter (LKB Wallac) as described by the supplier.

TABLE 5

250 ml Dulbecco's Modified Eagle's Medium (DMEM, Gibco-BRL)
250 ml Ham's F12 medium (Gibco-BRL)
0.29 mg/ml L-glutamine (Sigma, St. Louis, MO)
1 mM sodium pyruvate (Sigma, St. Louis, MO)
25 mM Hepes (Sigma, St. Louis, MO)
10 µg/ml fetuin (Aldrich, Milwaukee, WI)
50 µg/ml insulin (Gibco-BRL)
3 ng/ml selenium (Aldrich, Milwaukee, WI)
20 µg/ml transferrin (JRH, Lenexa, KS)

B.

Hearts were isolated from 1 day old neonatal mice and then disrupted by repeat collagenase digestions, following the protocol of Brand et al., (J. Biol. Chem. 268:11500-11503, 1993). Individual myocytes were isolated over a Percoll gradient, and 2 ml were plated in 6 well tissue cultrue dishes at 0.5 X 10^6 cells/ml. Three days later the wells were washed 3 times with PBS without calcium or magnesium, and refed with 1 ml serum free medium (Table 6). The wells were inoculated with 10^{11} particles AdCMV-zFGF5 per well or AdCMV-GFP (green fluorescent protein) as a control, and incubated at 37°C for 8 hours. The wells were then washed again 3 times with PBS without calcium or magnesium, and then refed with 2 mls serum free media.

Within 48 hours after inoculation with the AdCMV-zFGF5, the cultured myocytes have ceased to beat and have undergone a morphologic alteration, while the wells inoculated with the AdCMV-GFP continued to beat spontaneously and are unaffected morphologically by the inoculation. Wells incoulated with AdCMV-zFGF5 also contained, after 48, hours, a confluent layer of viable, non-adherent cells, without any loss in confluence of the

adherent myocyte layers, indicating the proliferative activity of the adCMV-zFGF5 on cultured murine myocytes.

Table 6

DMEM
Ham's Nutrient Mixture F12 (Gibco-BRL; 1:1 mixture with DMEM)
17 mM $NaHCO_3$ (Sigma)
2 mM L-glutamine (Sigma)
1% PSN (Sigma)
1 µg/ml insulin
5 µg/ml transferrin
1 nM LiCl (Sigma)
1 nM selenium
25 µg/ml ascorbic acid(Sigma)
1 nM thyroxine (Sigma)

C.

zFGF-5 fused to a maltose binding protein (MBP), as described in Example 9A and purified as described in Example 10, was added to myocytes (Example 3B) at a concentration of 0.1 ng/ml MBP-zFGF5 was shown to stimulate proliferation of myocytes, as well.

Example 4

Assay for *Ex Vivo* Activity of zFGF-5

Cardiac mitogenesis is measured *ex vivo* by removing entire hearts from neonatal or 8-week old mice or rats. The excised heart is placed in Joklik's (Sigma, St. Louis, MO) or Dulbecco's medium at 37°C, 5% CO_2 for 4-24 hours. During the incubation period zFGF-5 polypeptide is added at a concentration range of 1 pg/ml to 100 µg/ml. Negative controls are using buffer only. ^{3}H-thymidine is added and the samples are incubated for 1-4 hours, after which the heart is sectioned and mitogenesis is determined by autoradiography. Sections are used for histomorphometry to determine the nuclei/cytoplasmic volume (McLaughlin, Am. J. Physiol. 271:R122-R129, 1996.)

Alternatively, the heart was lyophilized and resuspended in 1 ml 0.1 N NaOH. The DNA was precipitated using ice cold 10% trichloroacetic acid (TCA). The supernatant was added to 9 ml scintillation fluid to measure non-specific ^{3}H-thymidine incorporation. The resulting pellet was resuspended in 1 ml BTS-450 tissue solubilizer (Beckman, Fullerton, CA) and added to 9 ml of scintillation fluid to measure specific DNA incorporation of ^{3}H-thymidine.

Left and right ventricles were isolated from isolated from 1 day old CD-1 mice (Jackson Labs, Bar Harbor, ME), and incubated for 4 hours with 3 ng/ml zFGF5Hep2 (n=13; see Example 10) or control (n=10). ^{3}H-thymidine was added for 1 hour. The ventricles were washed several times and then homogenized in 1 ml Joklik's medium. The resulting homogenate was added to 9 ml scintillation cocktail and analyzed for total ^{3}H-thymidine uptake and DNA incorporation.

zFGF5-Hep2 increased ^{3}H-thymidine uptake and incorporation in DNA 2.068 $\pm$ 0.489 fold over control, indicating that zFGF5 is mitogenic for a cardiac cell.

Example 5

Assay for *In Vivo* Activity of zFGF-5

The proliferative effects of zFGF-5 are assayed *in vivo* using two-week old neonatal rats and/or two-month old adult rats. The rats are injected intraperiocardially either acutely or chronically.

A.

Neonatal rats are treated with zFGF-5 for 1 to 14 days over a dose range of 50 ng/day to 100 µg/day. After treatment, the effects of zFGF-5 versus the sham-treated animals is evaluated by measuring increased cardiac weight, improved *in vivo* and *ex vivo* left ventricular function, and by increased cardiac nuclear to

cytosolic volume fractions, that are determined histomorphometrically.

B.

Rats with cardiomyopathy induced by chronic catecholamine infusion, by coronary ligation or for models of cardiomyopathy such as the Syrian Cardiomyopathic hamster (Sole et al., Amer. J. Cardiol. 62(11):20G-24G, 1988) are also used to evaluate the effects of zFGF-5 on cardiac function and tissue.

To induce cardiomyopathy using catecholamine, 7-8 week old rats are infused continuously with epinephrine for 2 weeks via osmotic minipumps implanted subcutaneously between their shoulder blades. The epinephrine infusion results in an increase in the left ventricular fibrotic lesion score from 0.005±0.005 to 2.11±0.18, scale from 0-3); increased left ventricular myocyte cell width from 17.36±0.46 μm to 23.05±0.62 μm; and negligible left ventricular papillary muscle contractile responses to isoproterenol (0.2 vs 1.1 grams tension compared to saline-infused rats. After the two week treatment period, the rats are injected intraperiocardially daily with either vehicle, zFGF-5, bFGF, IGF-I or IGF-II for up to 14 days. The rats are sacrificed and histomorphometry and histocytochemistry are performed.

Rats, treated as described above, are also evaluated at the end of the cathecholamine treatment, and again after growth factor treatment, where cardiac regeneration is measured as decreased left ventricular fibrotic lesion scores, reduced myocyte cell width and increased left ventricular papillary contractile responses to isoproterenol.

Example 6

Chromosomal Mapping of zFGF-5

ZFGF-5 was mapped to chromosome 5 using the commercially available version of the Whitehead

Institute/MIT Center for Genome Research's "GeneBridge 4 Radiation Hybrid Panel" (Research Genetics, Inc., Huntsville, AL). The GeneBridge 4 Radiation Hybrid Panel contains DNAs suitable for PCR use from each of 93 radiation hybrid clones, plus two control DNAs (the HFL donor and the A23 recipient). A publicly available WWW server (http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl) allows mapping relative to the Whitehead Institute/MIT Center for Genome Research's radiation hybrid map of the human genome (the "WICGR" radiation hybrid map) which was constructed with the GeneBridge 4 Radiation Hybrid Panel.

For the mapping of zFGF-5 with the "GeneBridge 4 RH Panel", 25 μl reactions were set up in a 96-well microtiter plate (Stratagene, La Jolla, CA) and used for PCR in a "RoboCycler Gradient 96" thermal cycler (Stratagene). Each of the 95 PCR reactions consisted of 2.5 μl 50X "Advantage KlenTaq Polymerase Mix" (Clontech), 2 μl dNTPs mix (2.5 mM each; Perkin-Elmer, Foster City, CA), 1.25 μl sense primer, ZC11,677 (SEQ ID NO: 4) 1.25 μl antisense primer, ZC12,053 (SEQ ID NO: 5).

2.5 μl "RediLoad" (Research Genetics, Inc), 0.5 μl "Advantage KlenTaq Polymerase Mix" (Clontech Laboratories, Inc.), .25 ng of DNA from an individual hybrid clone or control and ddH2O for a total volume of 25 μl. The reactions were overlaid with an equal amount of mineral oil and sealed. The PCR cycler conditions were as follows: an initial 1 cycle of 4 minutes at 94°C, 35 cycles of 1 minute at 94°C, 1.5 minute annealing at 66°C and 1.5 minute extension at 72°C, followed by a final 1 cycle extension of 7 minutes at 72°C. The reactions were separated by electrophoresis on a 3% NuSieve GTG agarose gel (FMC Bioproducts, Rockland, ME).

The results showed that zFGF-5 maps 541.12 cR from the top of the human chromosome 5 linkage group on the WICGR radiation hybrid map. Relative to the

centromere, its nearest proximal marker was WI-16922 and its nearest distal marker was WI-14692. The use of surrounding CHLC map markers also helped position zFGF-5 in the 5q34-q35 region on the CHLC chromosome 5 version v8c7 integrated marker map (The Cooperative Human Linkage Center, WWW server-http://www.chlc.org/ChlcIntegratedMaps.html).

Example 7

zFGF-5 Effects on Bone

A.

An adenovirus vector containing the cDNA for zFGF-5 was contructed using methods described by Becker et al. (Methods in Cell Biology 43:161-189, 1994). Briefly, the cDNA for zFGF-5 (as shown in SEQ ID NO: 1) was cloned as a Xba I-Sal I fragment into pACCMV (Gluzman et al., In Eucaryotic Viral Vectors, Gluzman (eds.) pp.187-192, Cold Spring Harbor Press, Cold Springs Harbor NY, 1982). The pACCMV vector contains part of the adenovirus 5 genome, the CMV promoter and an SV40 terminator sequence. The plasmid containing the vector and cDNA insert was cotransfected with a plasmid containing the the adenovirus 5 genome, designated pJM17, (McGrory et al., Virology 163:614-617, 1988) into 293 cells (ATCC No. CRL-1573; American Type Culture Collection, Rockville, MD), leading to a recombination event and the production of a recombinant adenovirus containing zFGF-5, designated AdCMV-zFGF5. The presence of the zFGF-5 cDNA was confirmed by PCR.

The adenovirus vector AdCMV-zFGF5 was used for gene tranfer *in vivo* by intravenous injection of between 1 X 10^{11} and 5 x 10^{11} particles/mouse. It has been shown that after intravenous injection, the majority of the virus targets the liver and very efficiently transduces hepatocytes (Herz et al., Proc. Natl. Acad. Sci. USA

90:2812-2816, 1993). It has been demonstrated that the cells produce the protein encoded by the cDNA, and in the case of secreted proteins, secret them into the circulation. High levels of expression and physiological effects have been demonstrated (Ohwada et al., Blood 88:768-774, 1996; Stevenson et al., Arteriosclerosis, Thrombosis and Vascular Biology, 15:479-484, 1995; Setoguchi et al., Blood 84:2946-2953, 1994; and Sakamoto et al., Proc. Natl. Acad. Sci. USA 91:12368-12372, 1994).

Six week old CD-1 mice (Jackson Labs, Bar Harbor, ME) were treated with adenovirus containing no cDNA insert (AdCMV-null) or AdCMV-zFGF5 either IV through the tail vein or intrapericardially (IPC). A total of 5 X 10^{11} viral particles/100 µl/mouse were given. 14 days after injection, the animals were sacrificed, and tibias and femurs were removed without being separated to examine any potential inflammatory response. The bones were fixed in 10% neutral buffered formalin and processed. They were decalcified in 5% formic acid with 10% sodium citrate, washed in water, dehydrated in a series of 70%-100% ethanol, cleared in xylene and embedded in paraffin. The specimens were cut longitudinally through both tibial and femoral metaphyses and stained with hemotoxylin and eosin for identification of bone cells. Osteoblasts were identified by central negative Golgi area and eccentric nucleus, while osteoclasts were identified by multinucleation, non-uniform shape and the Howship's lacunae associated with these resorbing cells.

For bone histomorphometry, femur samples were chosen. Cancellous bone volume was not measured due to variation in the sampling site (i.e., femur samples were not sectioned exactly at the same plane). Three bone parameters were evaluated for histomorphometric changes.

1. Number of endosteal osteoblasts: measured along the endosteal surface of cancellous bone at 180 X

magnification in an area 1.22 mm proximal to the growth plate.

2. Number of endosteal osteoclasts: measured along the endosteal surface of cancellous bone at 180 X magnification in an area 1.22 mm proximal to the growth plate.

3. Growth plate width: measured every 72 μm at 90 X magnification across the entire growth plate except at the peripheral ends to determine the growth plate activity.

Analyses of the data (mean ± SD, n=4-7/group) demonstrated the following:

1. There appeared to be no detectable inlfammatory response at the joint between tibia and femur.

2. AdCMV-zFGF5 given IV or IPC in mice significantly increased osteogenic activity in the distal femural metaphysis, when examined at 2 weeks. This stimulation of osteogenic activity was indicated by:

a) significant increases in the number of endosteal osteoblasts in the cancellous bone of distal femurs following IV infusion or IPC injection of AdCMV-zFGF5, 530% and 263%, respectively, when compared with their relative vector only controls; and

b) the observation of increased osteogenic tissues on the bone surface, suggesting increased differentiation of bone marrow stromal cells toward the osteoblast lineage.

3. The number of endosteal osteoclasts was not significantly affected by IV or IPC administration of AdCMV-zFGF5, when compared with their relative vector only controls.

4. The growth plate width was significantly decreased by IV infusion, but not IPC injection, of AdCMV-zFGF5, suggesting depressed growth plate activity

following IV infusion. The differential effects of AdCMV-zFGF5 administrations have not been elucidated.

These results suggest that zFGF-5 is a strong mitogen for stimulation of osteoblast proliferation and that zFGF-5 has the capacity to induce new bone formation.

B.

Using essentially the same procedures described above in 7.A. QCT was done on female CD-1 (Jackson Labs) that were injected with 1 $x10^{11}$ particles AdCMV-zFGF5 per mouse. The mice were sacrificed 30 days after injection and heart/tibial length ratios were increased compared to controls (injected with empty adenorvirus or saline). There were no differences between the groups in tibial lengths to account for the change, nor were there differences in any other organ weights among the groups. Thus, the indication is that zFGF-5 adenovirus selectively increases total bone density, trabecular bone density, and cortical thickness in the femur, as measured by QCT.

Example 8

Effects of zFGF-5 on Heart

As described in 7.B. CD-1 mice were given a single IV injection of AdCMV-zFGF5, sacrificed after four weeks, and the heart/tibial length ratios were found to be increased compared to empty adenovirus or saline treated mice. The results showed that there were no differences between the groups in tibial lengths to account for this change, nor were there differences in any other organ weights among the groups. This result suggests that AdCMV-zFGF5 selectively increased cardiac growth, when administered as an IV adenoviral construct.

Example 9

Expression of zFGF-5

A. Construction of zFGF5-Encoding Plasmids

zFGF5, a fibroblast growth factor homolog, was expressed in *E. coli* using the MBP (maltose binding protein) fusion system from New England Biolabs (NEB; Beverly, MA). In this system, the zFGF5 cDNA was attached to the 3' end of the malE gene to form an MBP-zFGF5 fusion protein. Fusion protein expression was driven by the tac promoter; expression is "off" until the promoter is induced by addition of 1 mmol IPTG (isopropyl b-thiogalactosylpyranoside). Three variations of this fusion protein were made, differing only in their cleavage site for liberating zFGF5 from MBP. One construct had a thrombin cleavage site engineered between the MBP and zFGF5 domains. The second construct had a Factor Xa cleavage site, instead of a thrombin cleavage site. The third construct had an enterokinase cleavage site, instead of the thrombin cleavage site.

The constructs were built as in-frame fusions with MBP in accordance with the Multiple Cloning Site (MCS) of the pMAL-c2 vector (NEB), and according to the manufacturer's specifications. zFGF5 was amplified via PCR using primers which introduced convenient cloning sites, as well as cleavage sites using the following oligonucleotide primers: 1) for the thrombin construct: zc12,652 (SEQ ID NO: 7) and zc12,631 (SEQ ID NO: 8); 2) for the Factor Xa construct: zc15,290 (SEQ ID NO: 9) and zc12,631 (SEQ ID NO: 8); and 3) for the enterokinase construct: zc15,270 (SEQ ID NO: 10) and zc12,631 (SEQ ID NO: 8). In each case, the native zFGF5 signal sequence was not amplified; the zFGF5 as expressed begins at amino acid residue 26 of SEQ ID NO: 2 (Val was changed to an Ala). The thrombin construct was built by inserting an Xba I-Sal I zFGF5 fragment into the Xba I-Sal I sites of pMAL-c2. The Factor Xa construct was built by inserting a blunt-Sal I fragment into the Xmn I-Sal I sites of the MCS. The enterokinase construct was built by inserting an Xba I-Sal I fragment into the Xba-Sal I sites of pMAL-c2.

Once the constructs were built, they were transformed into a variety of *E. coli* host strains and analyzed for high-level expression. The thrombin construct (designated pSDH90.5) was transfected into DH10B cells (GIBCO-BRL), while both the Factor Xa construct (designated pSDH117.3) and the enterokinase construct (designated pSDH116.3) were transfected into TOP10 cells (Invitrogen, San Diego, CA). All three MBP fusions are about 63kD (43kD in the MBP domain, and approximately 20kD in the zFGF5 domain).

B. Homologous Recombination/ zFGF5

Expression of zFGF5 in *Pichia methanolica* utilizes the expression system described in co-assigned PCT WO 9717450, incorporated herein by reference. An expression plasmid containing all or part of a polynucleotide encoding zFGF5 is constructed via homologous recombination. The expression vector is built from pCZR204, which contains the AUG1 promoter, followed by the αFpp leader sequence, followed by an amino-terminal peptide tag, a blunt-ended SmaI restriction site, a carboxy-terminal peptide tag, a translational STOP codon, followed by the AUG1 terminator, the ADE2 selectable marker, and finally the AUG1 3' untranslated region. Also included in this vector are the URA3 and CEN-ARS sequences required for selection and replication in *S. cerevisisiae*, and the Amp^R and colE1 ori sequences required for selection and replication in *E. coli*. The zFGF5 sequence inserted into this vector begins at residue 27 (Ala) of the zFGF amino acid sequence.

To construct pSDH114, a plasmid for expression of zFGF5 in *P. methanolica*, the following DNA fragments were transformed into *S. cerevisisae*: 100 ng of the 'acceptor vector' pCZR204 that has been digested with SmaI; 1 μg of an XbaI-SalI restriction fragment liberated from pSDH90.5 and encompassing zFGF5 coding sequence.; 1 μg of a synthetic, PCR-generated, double-stranded linker

segment that spans 70 base pairs of the aFpp coding sequence on one end and joins it to the 70 base pairs of the amino-terminus coding sequence from the mature zFGF5 sequence on the other was generated from the four oligonucleotides zc13,497 (SEQ ID NO: 11); zc15,131 (SEQ ID NO: 12); zc15,132; (SEQ ID NO: 18); zc15,134 (SEQ ID NO: 13), of which the sense strand of a double stranded sequence is shown in SEQ ID NO: 19 (5' linker sequence (aFpp -> zFGF5 N-terminus)) and 1 μg of of a synthetic, PCR-generated, double-stranded linker segment that spans 70 base pairs of carboxy terminus coding sequence from zFGF5 on one end with 70 base pairs of AUG1 terminator sequence was generated from the four oligonucleotides 13,529 (SEQ ID NO: 14); zc13,525 (SEQ ID NO: 15) zc13,526 (SEQ ID NO: 16); zc13,528 (SEQ ID NO: 17) of which the sense strand of a double stranded sense is shown in the SEQ ID NO: 20 (3' linker sequence (zFGF5 C-terminus -> *AUG1* terminator)). Ura^+ colonies were selected, and DNA from the resulting yeast colonies was extracted and transformed into *E. coli*. Individual clones harboring the correct expression construct were identified by PCR screening with oligonucleotides zc13,497 (SEQ ID NO: 11) and zc13,528 (SEQ ID NO: 12) followed by restriction digestion to verify the presence of the zFGF5 insert and DNA sequencing to confirm the desired DNA sequences had been enjoined with one another. Larger scale plasmid DNA is isolated for one of the correct clones, and the DNA is digested with Sfi I to liberate the *Pichia*-zFGF5 expression cassette from the vector backbone. The Sfi I-cut DNA is then transformed into a *Pichia methanolica* expression host, designated PMAD16, and plated on ADE D plates for selection. A variety of clones are picked and screened via Western blot for high-level zFGF5 expression.

More specifically, for small-scale protein production (e.g., plate or shake flask production), *P. methanolica* transformants that carry an expression

cassette comprising a methanol-regulated promoter (such as the *AUG1* promoter) are grown in the presence of methanol and the absence of interfering amounts of other carbon sources (e.g., glucose). For small-scale experiments, including preliminary screening of expression levels, transformants may be grown at 30°C on solid media containing, for example, 20 g/L Bacto-agar (Difco), 6.7 g/L yeast nitrogen base without amino acids (Difco), 10 g/L methanol, 0.4 mg/L biotin, and 0.56 g/L of -Ade -Thr -Trp powder. Because methanol is a volatile carbon source it is readily lost on prolonged incubation. A continuous supply of methanol can be provided by placing a solution of 50% methanol in water in the lids of inverted plates, whereby the methanol is transferred to the growing cells by evaporative transfer. In general, not more than 1 ml of methanol is used per 100-mm plate. Slightly larger scale experiments can be carried out using cultures grown in shake flasks. In a typical procedure, cells are cultivated for two days on minimal methanol plates as disclosed above at 30°C, then colonies are used to inoculate a small volume of minimal methanol media (6.7 g/L yeast nitrogen base without amino acids, 10 g/L methanol, 0.4 mg/L biotin) at a cell density of about 1 x 10^6 cells/ml. Cells are grown at 30°C. Cells growing on methanol have a high oxygen requirement, necessitating vigorous shaking during cultivation. Methanol is replenished daily (typically 1/100 volume of 50% methanol per day).

For production scale culturing, fresh cultures of high producer clones are prepared in shake flasks. The resulting cultures are then used to inoculate culture medium in a fermenter. Typically, a 500 ml culture in YEPD grown at 30°C for 1-2 days with vigorous agitation is used to inoculate a 5-liter fermenter. The cells are grown in a suitable medium containing salts, glucose, biotin, and trace elements at 28°C, pH 5.0, and >30%

dissolved O_2. After the initial charge of glucose is consumed (as indicated by a decrease in oxygen consumption), a glucose/methanol feed is delivered into the vessel to induce production of the protein of interest. Because large-scale fermentation is carried out under conditions of limiting carbon, the presence of glucose in the feed does not repress the methanol-inducible promoter.

Example 10

Purification of zFGF-5

E.coli fermentation medium was obtained from a strain expressing zfGF5 as a Maltose Binding protein fusion (pSDH90.5, as described above). The MBPzFGF5 fusion was solubilized during sonication or French press rupture, using a buffer containing 20 mM Hepes, 0.4 M Nacl, 0.01 M EDTA, 10 mM DTT, at pH 7.4. The extraction buffer also included 5 µg/ml quantities of Pepstatin, Leupeptin, Aprotinin, Bestatin. Phenyl methyl sulfonylfluoride (PMSF) was also included at a final concentration of 0.5 mM.

The extract was spun at 18,000 x g for 30 minutes at 4°C. The resulting supernatent was processed on an Amylose resin (Pharmacia LKB Biotechnology, Piscataway, NJ) which binds the MBP domain of the fusion. Upon washing the column, the bound MBPzFGF5 fusion was eluted in the same buffer as extraction buffer without DTT and protease inhibitors but containing 10 mM Maltose.

The eluted pool of MBPzFGF5 was treated with 1:100 (w/w) Bovine thrombin to MBPzFGF5 fusion. The cleavage reaction was allowed to proceed for 6 to 8 hours at room temperature, after which the reaction mixture was passed over a bed of Benzamidine sepharose (Pharmacia LKB Biotechnology, Piscataway, NJ) to remove the thrombin, using the same elution buffer as described above for Amylose affinity chromatography.

The passed fraction, containing the cleaved product zFGF5 and free MBP domain were applied to a Toso Haas Heparin affinity matrix (Toso Haas, Montgomeryville, PA) equilibrated in 0.5 M NaCl, 20 mM Hepes, 0.01 M EDTA at pH 7.4. The MBP and zFGF5 both bound to heparin under these conditions. The bound proteins were eluted with a 2 to 3 column volume gradient formed between 0.5M NaCl and 2.0 M NaCl in column buffer.

The MBP eluted early, at about 0.7 M NaCl, and the cleaved zFgf5 eluted at about 1.3 M NaCl. The pooled zFGF5 fractions were passed through the amylose step once again to remove any residual MBPzfgf5 that is a minor contaminant. The purified material was designated zFGF5-Hep2, and shows a single highly pure species at ~20 kDa on reducing SDS-PAGE analysis.

Amino acid N-terminal sequencing yielded the native N-Terminal sequence but Mass Spectrophotometry data revealed molecular masses indicating that the C-Terminus must be truncated at residue 196 (Lys) of SEQ ID NO: 2, where a "dibasic site" is present.

zFGF5 protein was very stable in 1.3 M NaCl. Upon dialysis into PBS, the zFGF5 aggregated and left the solution phase. Therefore,formulations that include heparin and other "polyanions" may be used to prevent the aggregation of pure zFGF5.

Example 11

Production of Antibodies

Antibodies for ZFGF5 were produced, using standard techniques known in the art and described previously, by immunizing guinea pigs, rabbits and mice with peptides QTRARDDVSRKQLRLYC (SEQ ID NO: 2 amino acid residue 40 to residue 56), designated zFGF-1; YTTVTKRSRRIRPTHRAC (SEQ ID NO: 2 amino acid residue 191 to residue 207, with an additional Cys at the C-terminus), designated zFGF-5 or the full-length zFGF5 polypeptide as

shown in SEQ ID NO: 2, plus the MPB fusion protein, and designated MBP-FGF5. Peptides were conjugated through Cys residues using Maleimide-activated KLH (Pierce Chemical Co., Rockford, IL).

Table 7 is a description of the animals, immunization levels and antibody separations.

Table 7

Peptide or Protein	animal	immun. level	Ab produced
ZFGF5-1	G.P.	50ug/animal initial 25ug/animal boost	Affinity purified and IgG fractionated.
	Rabbit	100ug/animal initial 50ug/animal boost	Affinity purified and IgG fractionated.
ZFGF5-2	G.P.	50ug/animal initial 25ug/animal boost	Affinity purified and IgG fractionated.
	Rabbit	100ug/animal initial 50ug/animal boost	Affinity purified. and IgG fractionated.
ZFGF5-MBP	Mouse	20ug/animal initial 10ug/animal boost	
	Rabbit	200ug/animal initial 100ug/animal boost	Affinity purified

Example 12

Effects of zFGF-5 on ob/ob Mice

The effects of zFGF-5 on adipocytes and fat metabolism were examined using female ob/ob mice (C57B1/6J, Jackson Labs, Bar Harbor, ME). The mice are obese, insulin resistant and have "fatty bone". The mice were weighed and all were found to be the same weight, and were injected IV with 10^{11} particles per mouse of AdCMVzFGF-5 or either saline or Ad5CMV-GFP for controls, as described in Example 7. 17 days after injection, the control mice injected with Ad5CMV-GFP had gained 5.342 ± 0.5 grams of body weight compared to the day of injection, while the AdCMVzFGF-5 treated mice lost 3.183 ±0.743 grams of body weight.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: ZymoGenetics, Inc.
1201 Eastlake Avenue East
Seattle,Washington 98102
United States of America

(ii) TITLE OF THE INVENTION: NOVEL FGF HOMOLOGS

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: ZymoGenetics, Inc.
(B) STREET: 1201 Eastlake Avenue East
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98102

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Sawislak, Deborah A
(B) REGISTRATION NUMBER: 37,438
(C) REFERENCE/DOCKET NUMBER: 96-20

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 206-442-6672
(B) TELEFAX: 206-442-6678
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 917 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...621
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
ATG TAT TCA GCG CCC TCC GCC TGC ACT TGC CTG TGT TTA CAC TTC CTG      48
Met Tyr Ser Ala Pro Ser Ala Cys Thr Cys Leu Cys Leu His Phe Leu
 1               5                  10                  15

CTG CTG TGC TTC CAG GTA CAG GTG CTG GTT GCC GAG GAG AAC GTG GAC      96
Leu Leu Cys Phe Gln Val Gln Val Leu Val Ala Glu Glu Asn Val Asp
            20                  25                  30

TTC CGC ATC CAC GTG GAG AAC CAG ACG CGG GCT CGG GAC GAT GTG AGC     144
Phe Arg Ile His Val Glu Asn Gln Thr Arg Ala Arg Asp Asp Val Ser
        35                  40                  45

CGT AAG CAG CTG CGG CTG TAC CAG CTC TAC AGC CGG ACC AGT GGG AAA     192
Arg Lys Gln Leu Arg Leu Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys
    50                  55                  60
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CAC ATC CAG GTC CTG GGC CGC AGG ATC AGT GCC CGC GGC GAG GAT GGG      240
His Ile Gln Val Leu Gly Arg Arg Ile Ser Ala Arg Gly Glu Asp Gly
65                  70                  75                  80

GAC AAG TAT GCC CAG CTC CTA GTG GAG ACA GAC ACC TTC GGT AGT CAA      288
Asp Lys Tyr Ala Gln Leu Leu Val Glu Thr Asp Thr Phe Gly Ser Gln
                85                  90                  95

GTC CGG ATC AAG GGC AAG GAG ACG GAA TTC TAC CTG TGC ATG AAC CGC      336
Val Arg Ile Lys Gly Lys Glu Thr Glu Phe Tyr Leu Cys Met Asn Arg
            100                 105                 110

AAA GGC AAG CTC GTG GGG AAG CCC GAT GGC ACC AGC AAG GAG TGT GTG      384
Lys Gly Lys Leu Val Gly Lys Pro Asp Gly Thr Ser Lys Glu Cys Val
        115                 120                 125

TTC ATC GAG AAG GTT CTG GAG AAC AAC TAC ACG GCC CTG ATG TCG GCT      432
Phe Ile Glu Lys Val Leu Glu Asn Asn Tyr Thr Ala Leu Met Ser Ala
    130                 135                 140

AAG TAC TCC GGC TGG TAC GTG GGC TTC ACC AAG AAG GGG CGG CCG CGG      480
Lys Tyr Ser Gly Trp Tyr Val Gly Phe Thr Lys Lys Gly Arg Pro Arg
145                 150                 155                 160

AAG GGC CCC AAG ACC CGG GAG AAC CAG CAG GAC GTG CAT TTC ATG AAG      528
Lys Gly Pro Lys Thr Arg Glu Asn Gln Gln Asp Val His Phe Met Lys
                165                 170                 175

CGC TAC CCC AAG GGG CAG CCG GAG CTT CAG AAG CCC TTC AAG TAC ACG      576
Arg Tyr Pro Lys Gly Gln Pro Glu Leu Gln Lys Pro Phe Lys Tyr Thr
            180                 185                 190

ACG GTG ACC AAG AGG TCC CGT CGG ATC CGG CCC ACA CAC CCT GCC TAGGC    626
Thr Val Thr Lys Arg Ser Arg Arg Ile Arg Pro Thr His Pro Ala
        195                 200                 205

CACCCCGCCG CGGCCCTCAG GTCGCCCTGG CCACACTCAC ACTCCCAGAA AACTGCATCA    686
GAGGAATATT TTTACATGAA AAATAAGGAT TTTATTGTTG ACTTGAAACC CCCGATGACA    746
AAAGACTCAC GCAAAGGGAC TGTAGTCAAC CCACAGGTGC TTGTCTCTCT CTAGGAACAG    806
ACAACTCTAA ACTCGTCCCC AGAGGAGGAC TTGAATGAGG AAACCAACAC TTTGAGAAAC    866
CAAAGTCCTT TTTCCCAAAG GTTCTGAAAA AAAAAAAAAA AAAAACTCGA G              917
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Tyr Ser Ala Pro Ser Ala Cys Thr Cys Leu Cys Leu His Phe Leu
 1               5                  10                  15
Leu Leu Cys Phe Gln Val Gln Val Leu Val Ala Glu Glu Asn Val Asp
            20                  25                  30
Phe Arg Ile His Val Glu Asn Gln Thr Arg Ala Arg Asp Asp Val Ser
        35                  40                  45
Arg Lys Gln Leu Arg Leu Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys
    50                  55                  60
His Ile Gln Val Leu Gly Arg Arg Ile Ser Ala Arg Gly Glu Asp Gly
65                  70                  75                  80
Asp Lys Tyr Ala Gln Leu Leu Val Glu Thr Asp Thr Phe Gly Ser Gln
                85                  90                  95
Val Arg Ile Lys Gly Lys Glu Thr Glu Phe Tyr Leu Cys Met Asn Arg
            100                 105                 110
Lys Gly Lys Leu Val Gly Lys Pro Asp Gly Thr Ser Lys Glu Cys Val
        115                 120                 125
Phe Ile Glu Lys Val Leu Glu Asn Asn Tyr Thr Ala Leu Met Ser Ala
    130                 135                 140
Lys Tyr Ser Gly Trp Tyr Val Gly Phe Thr Lys Lys Gly Arg Pro Arg
145                 150                 155                 160
Lys Gly Pro Lys Thr Arg Glu Asn Gln Gln Asp Val His Phe Met Lys
                165                 170                 175
Arg Tyr Pro Lys Gly Gln Pro Glu Leu Gln Lys Pro Phe Lys Tyr Thr
            180                 185                 190
Thr Val Thr Lys Arg Ser Arg Arg Ile Arg Pro Thr His Pro Ala
        195                 200                 205
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC11676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGACTTGACT ACCGAAGGTG TCTG 24

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC11677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCGATGTGA GCCGTAAGCA GCT 23

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC12053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCATACTTGT CCCCATCCTC GCCGCG 26

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 621 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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CARGTNCARG TNYTNGTNGC NGARGARAAY GTNGAYTTYM GNATHGAYGT NGARAARCAR 120
ACNMGNGCNM GNGAYGAYGT NWSNMGNAAR CARYTNMGNY TNTAYCARYT NTAYWSNMGN 180
ACNWSNGGNA ARCAYATHCA RGTNYTNGGN MGNMGNATHW SNGCNMGNGG NGARGAYGGN 240
GAYAARTAYG CNCARYTNYT NGTNGARACN GAYACNTTYG GNWSNCARGT NMGNATHAAR 300
GGNAARGARA CNGARTTYTA YYTNTGYATG AAYMGNAARG GNAARYTNGT NGGNAARCCN 360
GAYGGNACNW SNAARGARTG YGTNTTYATH GARAARGTNY TNGARAAYAA YTAYACNGCN 420
YTNATGWSNG CNAARTAYWS NGGNTGGTAY GTNGGNTTYA CNAARAARGG NMGNCCNMGN 480
AARGGNCCNA ARACNMGNGA RAAYCARCAR GAYGTNCAYT TYATGAARMG NTAYCCNAAR 540
GGNCARCCNG ARYTNCARAA RCCNTTYAAR TAYACNACNG TNACNAARMG NWSNMGNMGN 600
ATHMGNCCNA CNCAYCCNGC N 621

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC12652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TATTTATCTA GACTGGTTCC GCGTGCCGCC GAGGAGAACG TGGACTT 47

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC12631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTATTTGTCG ACTCAGGCAG GGTGTGTGGG CCG 33

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC15290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCCGAGGAGA ACGTGGACTT CC 22

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC15270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TATTTATCTA GAGATGACGA TGACAAGGCC GAGGAGAACG TGGACTT 47

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC13497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCATTGCTA AAGAAGAAGG TGTAAGCTTG GACAAGAGAG A 41

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC15131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTGTAAGCT TGGACAAGAG AGAGGAGAAC GTGGACTTCC GCATCCACGT GGAGAACCAG 60
ACG 63

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC15134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCGGCTGTAG AGCTGGTACA GCCGCAGCTG CTTACGGCT 39

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC13529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTTCACAAGC CCTTCAAGTA CACGACGGTG ACCAAGAGGT CC 42

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC13525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACGACGGTGA CCAAGAGGTC CCGTCGGATC CGGCCCACAC ACCCTGCCTA GGGGGAATTC 60
G 61

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC13526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CAAACAGGCA GCCCTAGAAT ACTAGTGTCG ACTCGAGGAT CCGAATTCCC CCTAGGCAGG 60
G 61

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC13528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTCAAAAATT ATAAAAATAT CCAAACAGGC AGCCCTAGAA TACT 44

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: ZC15132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAGCCGCAGC TGCTTAGCGC TCACATCGTC CCGAGCCCGC GTCTGGTTCT CCACGTGGAT GC 62

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCATTGCTG CTAAAGAAGA AGGTGTAAGC TTGGACAAGA GAGAGGAGAA CGTGGACTTC 60
CGCATCCACG TGGAGAACCA GACGCGGGCT CGGGACGATG TGAGCCGTAA GCAGCTGCGG 120
CTGTACCAGC TCTACAGCCG G 141

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTTCAGAAGC CCTTCAAGTA CACGACGGTG ACCAAGAGGT CCCGTCGGAT CCGGCCCACA 60
CACCCTGCCT AGGGGGAATT CGGATCCTCG AGTCGACACT AGTATTCTAG GGCTGCCTGT 120
TTGGATATTT TTATAATTTT TGAG 144

CLAIMS

We claim:

1. An isolated polynucleotide molecule encoding a fibroblast growth factor (FGF) homolog polypeptide selected from the group consisting of:

a) polynucleotide molecules comprising a nucleotide sequence as shown in SEQ ID NO: 1 from nucleotide 82 to nucleotide 621;

b) allelic variants of (a);

c) polynucleotide molecules that encode a polypeptide that is at least 60% identical to the amino acid sequence of SEQ ID NO: 2 from amino acid residue 28 (Glu) to amino acid residue 207 (Ala); and

d) polynucleotide molecules comprising a nucleotide sequence as shown in SEQ ID NO: 6 from nucleotide 82 to nucleotide 621.

2. The isolated polynucleotide molecule of claim 1, wherein the polynucleotide molecule comprises a nucleotide sequence as shown in SEQ ID NO: 1 from nucleotide 1 to nucleotide 621 or a nucleotide sequence as shown in SEQ ID NO: 6 from nucleotide 1 to nucleotide 621.

3. The isolated polynucleotide molecule of claim 1, wherein the polynucleotide molecule comprises a nucleotide sequence as shown in SEQ ID NO: 1 from nucleotide 82 to nucleotide 621.

4. The isolated polynucleotide molecule of claim 1, wherein the polynucleotide is DNA.

5. An expression vector comprising the following operably linked elements:

a transcription promoter;

a DNA segment selected from the group consisting of:

a) polynucleotide molecules comprising a nucleotide sequence as shown in SEQ ID NO: 1 from nucleotid 82 to nucleotide 621;

b) allelic variants of (a);

c) polynucleotide molecules that encode a polypeptide that is at least 60% identical to the amino acid sequence of SEQ ID NO: 2 from amino acid residue 28 (Glu) to amino acid residue 207 (Ala); and

d) polynucleotide molecules comprising a nucleotide sequence as shown in SEQ ID NO: 6 from nucleotide 82 to nucleotide 621; and

a transcription terminator.

6. A cultured cell into which has been introduced an expression vector according to claim 5, wherein said cell expresses a polypeptide encoded by the DNA segment.

7. A method of producing an FGF homolog polypeptide comprising:

culturing a cell into which has been introduced an expression vector according to claim 5, whereby said cell expresses a FGF homolog polypeptide encoded by the DNA segment; and

recovering the FGF homolog polypeptide.

8. An isolated FGF homolog polypeptide selected from the group consisting of:

a) polypeptide molecules comprising an amino acid sequence as shown in SEQ ID NO: 2 from residue 28 (Glu) to residue 175 (Met);

b) allelic variants of (a); and

c) polypeptide molecules that are at least 60% identical to SEQ ID NO: 2 from amino acid residue 28 (Glu) to amino acid residue 175 (Met).

9. An isolated FGF homolog polypeptide selected from the group consisting of:

a) polypeptide molecules comprising an amino acid sequence as shown in SEQ ID NO: 2 from residue 28 (Glu) to residue 196 (Lys);

b) allelic variants of (a); and

c) polypeptide molecules that are at least 60% identical to SEQ ID NO: 2 from amino acid residue 28 (Glu) to amino acid residue 196 (Lys).

10. An isolated FGF homolog polypeptide selected from the group consisting of:

a) polypeptide molecules comprising an amino acid sequence as shown in SEQ ID NO: 2 from residue 28 (Glu) to residue 207 (Ala);

b) allelic variants of (a); and

c) polypeptide molecules that are at least 60% identical to the amino acids of SEQ ID NO: 2 from amino acid residue 28 (Glu) to amino acid residue 207 (Ala).

11. The FGF homolog polypeptide of claim 8 further comprising a signal sequence.

12. The FGF homolog polypeptide of claim 8 further comprising a signal sequence as shown in SEQ ID NO: 2 from amino acid residue 1 (Met) to amino acid residue 27 (Ala).

13. A pharmaceutical composition comprising a purified FGF homolog polypeptide according to claim 8, in combination with a pharmaceutically acceptable vehicle.

14. An antibody that binds to an epitope of a polypeptide molecule comprising an amino acid sequence as shown in SEQ ID NO: 2 from residue 1 (Met) to residue 207 (Ala).

15. The antibody of claim 14 that binds a polypeptide molecule comprising an amino acid sequence a. shown in SEQ ID NO: 2 from residue 28 (Glu) to residue 196 (Lys).

16. A method of stimulating proliferation of myocytes or myocyte progenitors comprising administering to a mammal in need thereof, an amount of an FGF homolog polypeptide sufficient to produce a clinically significant increase in the number of myocytes or myocyte progenitors in said mammal.

17. The method of claim 16, wherein the myocytes or myocyte progenitors are cardiac myocytes or cardiac myocytes progenitors.

18. A method for *ex vivo* stimulation of myocyte progenitor cells or myocytes comprising culturing heart tissue cells with an amount of an FGF homolog polypeptide sufficient to produce an increase in the number of myocyte progenitor cells or myocytes in the heart tissue cells cultured in the presence of an FGF homolog polypeptide, as compared to heart tissue myocyte progenitor cells or myocytes cultured in the absence of an FGF homolog polypeptide.

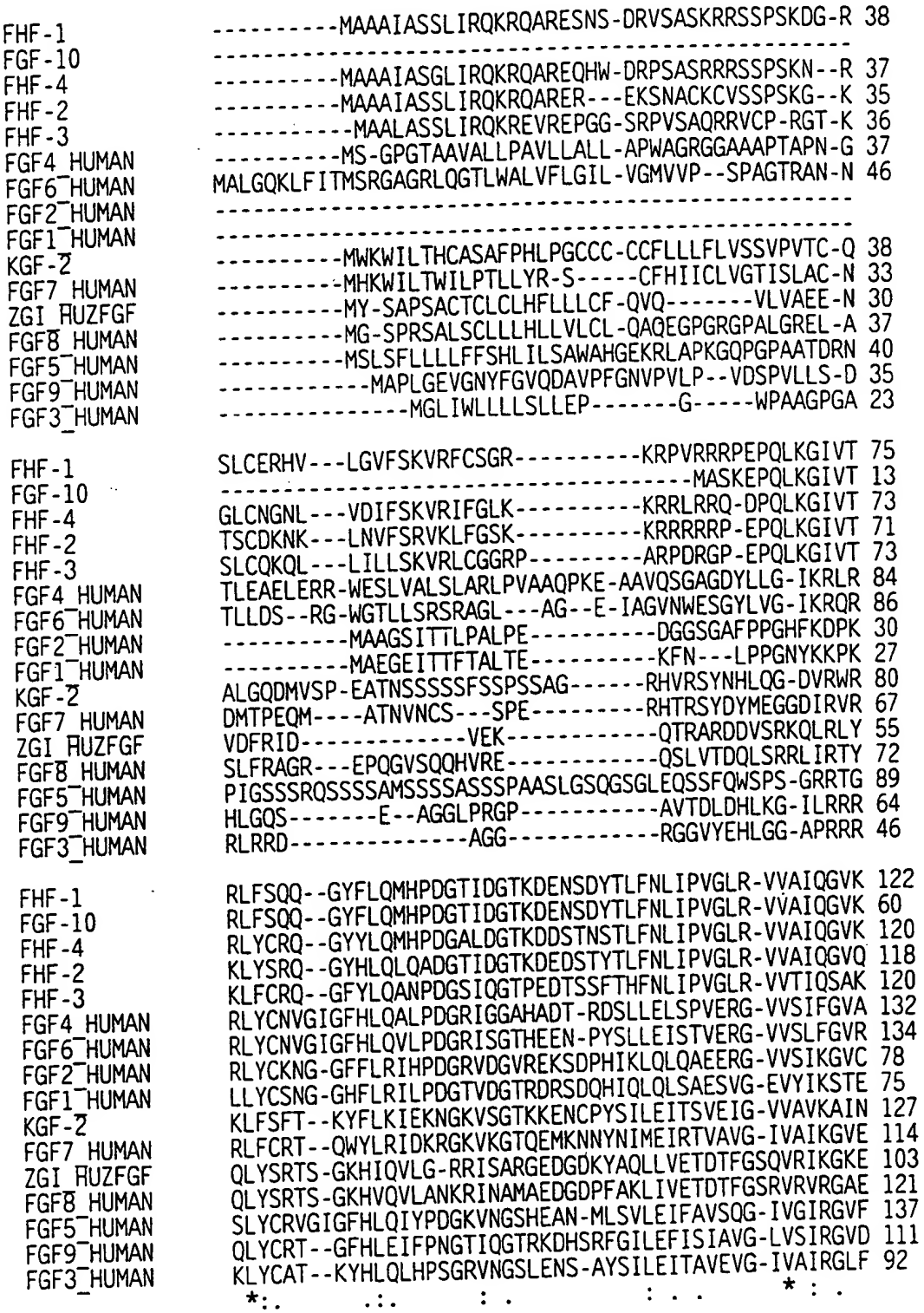
19. The method of claim 18, wherein the myocytes or myocyte progenitors are cardiac myocytes or cardiac myocytes progenitors.

20. A method of delivering an agent or drug selectively to heart tissue comprising:

linking a first molecule comprising an FGF homolog polypeptide with a second molecule comprising an agent or drug to form a chimera; and

administering the chimera to heart tissue.

Fig. 1/3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FHF-1 SLCERHV---LGVFSKVRFCSGR----------KRPVRRRPEPQLKGIVT 75
FGF-10 ----------MASKEPQLKGIVT 13
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FHF-2 TSCDKNK---LNVFSRVKLFGSK----------KRRRRRP-EPQLKGIVT 71
FHF-3 SLCQKQL---LILLSKVRLCGGRP---------ARPDRGP-EPQLKGIVT 73
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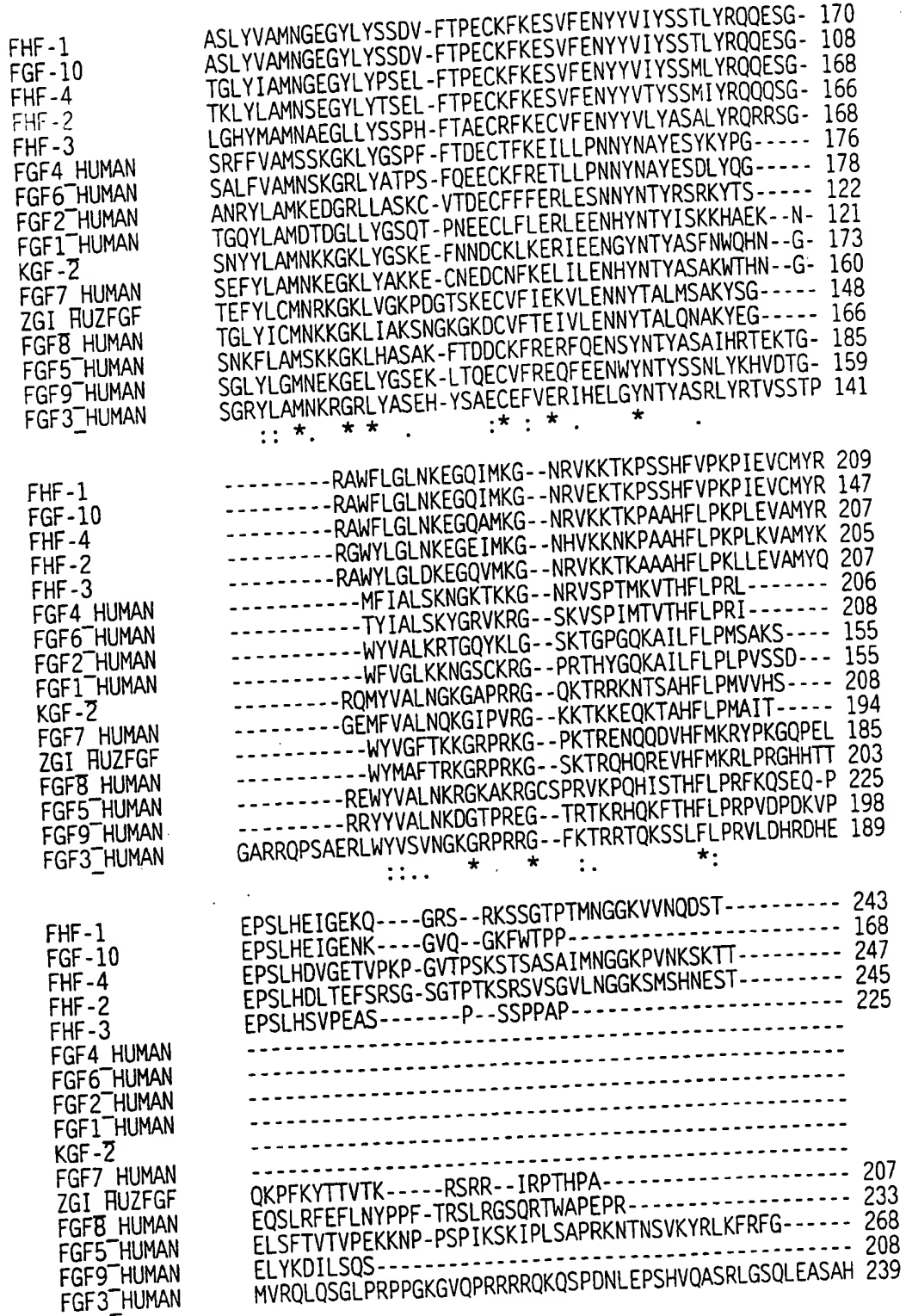
Fig. 1

Fig. 2/3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FGF8_HUMAN TGLYICMNKKGKLIAKSNGKGKDCVFTEIVLENNYTALQNAKYEG----- 166
FGF5_HUMAN SNKFLAMSKKGKLHASAK-FTDDCKFRERFQENSYNTYASAIHRTEKTG- 185
FGF9_HUMAN SGLYLGMNEKGELYGSEK-LTQECVFREQFEENWYNTYSSNLYKHVDTG- 159
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EPSLHSVPEAS-------P--SSPPAP---------- 225
---------- 207
QKPFKYTTVTK-----RSRR--IRPTHPA---------- 233
EQSLRFEFLNYPPF-TRSLRGSQRTWAPEPR---------- 268
ELSFTVTVPEKKNP-PSPIKSKIPLSAPRKNTNSVKYRLKFRFG------ 208
ELYKDILSQS---------- 239
MVRQLQSGLPRPPGKGVQPRRRRQKQSPDNLEPSHVQASRLGSQLEASAH

Fig. 2

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	1.00	0.39	0.43	0.29	0.46	0.33	0.36	0.38	0.37	0.41	0.39	0.40	0.42	0.40	0.35	0.38
2		1.00	0.38	0.34	0.41	0.35	0.38	0.33	0.38	0.44	0.39	0.37	0.37	0.39	0.35	0.60
3			1.00	0.31	0.42	0.34	0.33	0.36	0.34	0.38	0.35	0.37	0.41	0.46	0.35	0.35
4				1.00	0.34	0.53	0.26	0.24	0.26	0.31	0.28	0.30	0.30	0.31	0.28	0.32
5					1.00	0.35	0.39	0.43	0.39	0.39	0.43	0.42	0.44	0.43	0.40	0.43
6						1.00	0.33	0.31	0.33	0.31	0.32	0.34	0.34	0.32	0.36	0.36
7							1.00	0.34	0.98	0.33	0.76	0.81	0.34	0.37	0.67	0.42
8								1.00	0.34	0.54	0.34	0.37	0.36	0.36	0.34	0.38
9									1.00	0.33	0.66	0.72	0.34	0.37	0.62	0.42
10										1.00	0.32	0.35	0.40	0.37	0.32	0.43
11											1.00	0.68	0.36	0.38	0.58	0.41
12												1.00	0.36	0.33	0.62	0.42
13													1.00	0.47	0.34	0.32
14														1.00	0.30	0.31
15															1.00	0.38
16																1.00

Fig. 3

INTERNATIONAL SEARCH REPORT

Interna[illegible]nal Application No
PCT/US 97/18635

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/18 C07K14/50 C07K16/22 C07K19/00 C12N5/10
A61K38/18

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	LONG CS ET AL: "A growth factor for cardiac myocytes is produced by cardiac nonmyocytes." CELL REGUL, DEC 1991, 2 (12) P1081-95, UNITED STATES, XP002052685 see the whole document ---	16-19
A	CROSSLEY PH ET AL: "Roles for FGF8 in the induction, initiation, and maintenance of chick limb development." CELL, JAN 12 1996, 84 (1) P127-36, UNITED STATES, XP002052686 see the whole document ---	1,5-8
	-/--	

[X] Further documents are listed in the continuation of box C.

[ ] Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

2

Date of the actual completion of the international search	Date of mailing of the international search report
20 January 1998	2.0. 02. 98
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Authorized officer Gurdjian, D

Form PCT/ISA/210 (second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

Interna nal Application No
PCT/US 97/18635

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	GOLDFARB M: "The fibroblast growth factor family." CELL GROWTH DIFFER, SEP 1990, 1 (9) P439-45, UNITED STATES, XP002052687 see the whole document	1,5-8

INTERNATIONAL SEARCH REPORT

Inte ional application No.
PCT/US 97/18635

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

see FURTHER INFORMATION sheet PCT/ISA/210

2. [ ] Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [ ] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Remark : Although claims 16 ,17 ,20 are directed to a method of treatment of the human/animal body , the search has been carried out and based on the alleged effects of the compound/composition.